

GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: December 18, 2003, 15:27:15 ; Search time 17 Seconds

CY (without alignments)  
1421.866 Million cell updates/sec

Title: NP418220

Perfect score: 2633  
Sequence: 1 MADSQLPSCAPEGAEYLRAY.....LGYDCHDETNPAPRFPLAG 514

Scoring table: BIOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2633	100.0	514	1	THD1_ECOLI
2	2525	95.9	514	1	THD1_SALTY
3	1857.5	70.5	513	1	THD1_PASNU
4	1738.5	66.0	513	1	THD1_HAEIN
5	1383	52.5	507	1	THD1_BURCE
6	1212.5	46.1	576	1	THDH_YEAST
7	1136	43.1	550	1	THDH_ARXAD
8	1087	41.3	592	1	THD1_ARATH
9	994.5	37.8	595	1	THD1_LYCES
10	937.5	35.6	590	1	THD1_CICAR
11	642	24.4	359	1	THD1_SOLRU
12	642	24.4	422	1	THD1_BACSU
13	608	23.1	415	1	THD1_BACHD
14	600	22.8	416	1	THD1_LACLA
15	578.5	22.0	429	1	THD1_MYCTU
16	577	21.9	427	1	THD1_MYCLE
17	566	21.5	436	1	THD1_CORGL
18	534	20.3	329	1	THD2_SALTY
19	529	20.1	329	1	THD2_ECOLI
20	485	18.4	326	1	YKX8_YEAST
21	470	17.9	323	1	YKNE_YEAST
22	466	17.7	332	1	YATJ_RHIN
23	378	14.4	339	1	SRR_MOUSE
24	357	13.6	340	1	SRR_HUMAN
25	308	11.7	328	1	SDHL_HUMAN
26	279	10.6	362	1	SDHL_RAT
27	232.5	8.8	307	1	CYSK_FLAAP
28	230	8.7	307	1	CYSK_BACSU
29	228.5	8.7	338	1	SDHL_YEAST
30	225.5	8.6	360	1	STDH_YEAST
31	221.5	8.4	405	1	THRC_METUA
32	215.5	8.2	352	1	THRC_BACSP
33	211.5	8.0	404	1	DPAL_SALTY

34	209.5	8.0	352	1	THRC_BACSU	P04990 bacillus su
35	208	7.9	354	1	THRC_BACHD	Q9K763 bacillus ha
36	208	7.9	398	1	DPAL_ECOLI	Q46804 escherichia
37	194.5	7.4	310	1	CYSK_MYCTU	P95230 mycobacteri
38	186	7.1	311	1	CYSM_BACSU	O34476 bacillus su
39	186	7.1	325	1	CTK2_ORYSA	Q3X66 oryza sativ
40	183.5	7.0	299	1	CYSM_CAMJE	P71128 campylobact
41	177.5	6.7	310	1	CYSK_MYCLE	O32978 mycobacteri
42	176.5	6.7	392	1	CYSL_ARATH	P47999 arabidopsis
43	174	6.6	325	1	CYSK_SPIOL	O00834 spiniacia ol
44	173.5	6.6	325	1	CYSK_WHEAT	P38076 triticum ae
45	172	6.5	382	1	THRC_SINY3	P74193 synecchocyst

## ALIGNMENTS

RESULT 1  
ID THD1\_ECOLI STANDARD, FRF, 514 AA.  
AC \* P04968:  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Threonine dehydratase biosynthetic (EC 4.3.1.19) (Threonine  
deaminase).  
GN ILVA OR B3772.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=86056322; PubMed=3315862;  
RA Cox J.L., Cox B.J., Fidanza V., Calhoun D.H.,  
RT "The complete nucleotide sequence of the livGMEBA cluster of  
RL Escherichia coli K-12." ;  
RN Gene 56:185-198(1987).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Garrison E., Harms E., Umbarger H.E.,  
RT "The complete nucleotide sequence of the livGMEBA cluster of  
RL Escherichia coli K-12." ;  
RN Hatfield G.W.,  
RA "The complete nucleotide sequence of the livGMEBA operon of  
RL Escherichia coli K-12." ;  
RN Nucleic Acids Res. 15:2137-2155(1987).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=92358234; PubMed=1379743;  
RA Daniels D.L., Plunkett G., III, Burland V.D., Blattner F.R.,  
RT "Analysis of the Escherichia coli genome: DNA sequence of the region  
RN from 84.5 to 86.5 minutes." ;  
RL Science 257:771-778(1992).  
RN [5]  
RP SEQUENCE OF 439-514 FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=86111952; PubMed=3003115;  
RA Wek R.C., Hatfield G.W.,  
RT "Nucleotide sequence and in vivo expression of the livY and livC  
RN genes in Escherichia coli K12. Transcription from divergent  
RT overlapping promoters." ;  
RL J. Biol. Chem. 261:2441-2450(1986).  
RN [6]  
RP SEQUENCE OF 1-10 FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=89326124; PubMed=2473940;

RA Lopes J.M., Lawther R.P.,  
RT "Physical identification of an internal promoter, ilvP, in the  
RT distal portion of the ilvGEMDA operon.",  
RL Gene 76:255-269 (1989).  
RN [7]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
RX MEDLINE=98230745; PubMed=9562556;  
RA Gallagher D.T., Gilliland G.L., Xiao G., Zondlo J., Fisher K.E.,  
RA Chinchilla D., Eisenstein E.,  
RT "Structure and control of pyridoxal phosphate dependent allosteric  
RT threonine deaminase.",  
RL Structure 6:465-475 (1998).  
CC -1- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from  
CC threonine in a two-step reaction. The first step is a dehydration  
CC of threonine, followed by rehydration and liberation of ammonia.  
CC Deaminates L-threonine, but also L-serine to a lesser extent.  
CC -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).  
CC -1- COFACTOR: Pyridoxal phosphate.  
CC -1- ENZYME REGULATION: ISOLEUCINE ALLOSTERICALLY INHIBITS WHEREAS  
CC VALINE ALLOSTERICALLY ACTIVATES THIS ENZYME.  
CC -1- PATHWAY: Isoleucine biosynthesis; first step.  
CC -1- SUBUNIT: Homotrimer.  
CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.  
CC -----  
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CC -----  
DR EMBL: X04890; CAA28577.1; -  
DR EMBL: K03503; AAA24014.1; -  
DR EMBL: M10313; AAB59054.1; -  
DR EMBL: M11689; AAA24027.1; -  
DR EMBL: M32253; AAA24024.1; -  
DR EMBL: M87049; AAA67575.1; -  
DR EMBL: AE000453; AAC7492.1; -  
DR EMBL: M25497; AAA24015.1; -  
DR PIR: B27310; DMECTS.  
DR PDB: 1TDJ; 18-NOV-98.  
DR ECO2DBASE; F050.1; 6TH EDITION.  
DR EcoGene; EG10493; ilvA.  
DR InterPro: IPR001926; B6 enzyme beta.  
DR InterPro: IPR000634; S/T dehydratase.  
DR InterPro: IPR005787; Thz dehydratase.  
DR InterPro: IPR001721; ThzDh\_C.  
DR Pfam; PF00291; PALP; 1.  
DR Pfam; PF00585; Thz dehydratase C; 2.  
DR TIGRFAMs; TIGR01124; ilvA\_2Cterm; 1.  
DR PROSITE; PS00165; DEHYDRATASE\_SER\_THR; 1.  
DR Isoleucine biosynthesis; lyase; pyridoxal phosphate;  
KW Allosteric enzyme; 3D-structure; Complete proteome.  
KW BINDING  
FT FT 120 120 A -> R (IN REF. 2).  
FT FT 140 140 A -> R (IN REF. 2).  
FT FT 195 195 G -> C (IN REF. 2).  
FT FT 243 243 A -> G (IN REF. 3).  
FT FT 334 334 G -> V (IN REF. 2).  
FT FT 6 7  
FT FT 13 22  
FT FT 25 27  
FT FT 28 28  
FT STRAND 34 36  
FT FT 38 43  
FT FT 44 45  
FT FT 47 51  
FT FT 53 55  
FT FT 57 58  
FT FT 62 62  
FT FT 63 71  
FT FT 72 75

FT STRAND 83 86  
FT FT HELIX 91 100  
FT FT TURN 101 102  
FT STRAND 105 108  
FT FT HELIX 115 124  
FT STRAND 127 129  
FT FT HELIX 135 149  
FT STRAND 152 153  
FT FT HELIX 160 176  
FT FT TURN 178 179  
FT STRAND 182 186  
FT FT HELIX 191 203  
FT FT TURN 205 206  
FT STRAND 208 214  
FT FT TURN 215 217  
FT FT HELIX 219 226  
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FT FT HELIX 419 421  
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FT STRAND 434 439  
FT FT TURN 444 445  
FT FT HELIX 446 454  
FT FT STRAND 462 464  
FT FT TURN 466 466  
FT FT STRAND 475 479  
FT FT STRAND 498 501  
FT FT TURN 503 504  
FT FT HELIX 506 511  
FT FT TURN 512 512  
SQ SEQUENCE 514 AA; 56135 MW; 9D389A0EDD8DE92 CRC64;  
Query Match 100.0%; Score 2633; DB 1; Length 514;  
Best Local Similarity 99.6%; Pred. No. 1,4e-170;  
Matches 512; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MADSPPLSGAPGAEYLRVLRAPVYEAQVTPLOQMELSSRLDNVILVKEDRQPVHS 60  
DB 1 MADSPPLSGAPGAEYLRVLRAPVYEAQVTPLOQMELSSRLDNVILVKEDRQPVHS 60  
QY 61 FKLRGAYMMAGLTTEBQKAGVITASAGNHAQVAFSSARLGVKALITMPTATADIKVDA 120  
DB 61 FKLRGAYMMAGLTTEBQKAGVITASAGNHAQVAFSSARLGVKALITMPTATADIKVDA 120  
QY 121 VRGFGGVLLHGANPDEAKAKAIELSQOQGFVWPPEFDPMTIAGOGTALTELQODAH 180  
DB 121 VRGFGGVLLHGANPDEAKAKAIELSQOQGFVWPPEFDPMTIAGOGTALTELQODAH 180

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OY 181 DRVFPVGGGGLAAGVAVLILKQMLPQIVIAVEADSDACLKAAADAGHPVDLPRVGLFAE 240
DB 181 DRVFPVGGGGLAAGVAVLILKQMLPQIVIAVEADSDACLKAAADAGHPVDLPRVGLFAE 240
OY 241 GVAVKRIDETFRLLCOEYLDDIITVDSDAICAMKDLFEDVRAVAEPGALALAGMKYI 300
DB 241 GVAVKRIDETFRLLCOEYLDDIITVDSDAICAMKDLFEDVRAVAEPGALALAGMKYI 300
OY 301 ALHNHGRRLAHITISGANVNFHGLRYVSEBCELBORFALLAVTIPKSGFLKFCOLLG 360
DB 301 ALHNHGRRLAHITISGANVNFHGLRYVSEBCELBORFALLAVTIPKSGFLKFCOLLG 360
OY 361 GRSVTEFNRYRPAADAKNACIFVGVRLSRGLSEKKEILLQMLNDGYSVDLSDEMAKLVHR 420
DB 361 GRSVTEFNRYRPAADAKNACIFVGVRLSRGLSEKKEILLQMLNDGYSVDLSDEMAKLVHR 420
OY 421 YWVGSRPSHPLQERLYSEFPESPGAKLRFNLTLGTWNISLFHYRSHGTDYGRVLAPE 480
DB 421 YWVGSRPSHPLQERLYSEFPESPGAKLRFNLTLGTWNISLFHYRSHGTDYGRVLAPE 480
OY 481 XGDHPDEPTRLNELGYDCHDENTNPAFRFLAG 514
DB 481 XGDHPDEPTRLNELGYDCHDENTNPAFRFLAG 514

RESULT 2
ID THDI_SALTY STANDARD; PRT; 514 AA.
AC P20506; Q9L6S8;
DT 01-FEB-1991 (Rel. 17, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Threonine dehydratase biosynthetic (EC 4.3.1.19) (Threonine
  deaminase).
GN ILVA OR STM3905 OR STM01.87.
OS Salmoneilla typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Salmoneilla.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88255870; PubMed=3290055;
RA Tallon B.E., Little R., Lawther R.P.;
RT "Analysis of the functional domains of biosynthetic threonine
  deaminase by comparison of the amino acid sequences of three
  wild-type alleles to the amino acid sequence of biodegradative
  threonine deaminase."
RT Gene 63:245-252(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
  Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
  Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvaney E.,
  Ryan E., Sun H., Flores L., Miller W., Stonking T., Nhan M.,
  Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmoneilla enterica serovar Typhimurium
  LT2."
RT Nature 413:852-856(2001).
RN [3]
RP SEQUENCE OF 1-10 FROM N.A.
RX STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=89326124; PubMed=2473940;
RA Lopes J.M., Lawther R.P.;
RT "Physical identification of an internal promoter, ilvP, in the
  distal portion of the ilvGMDA operon."
RT Gene 76:255-269(1989).
CC -!- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from
  threonine in a two-step reaction. The first step is a dehydratation
  of threonine, followed by rehydration and liberation of ammonia.
CC -!- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
CC -!- COFACTOR: Pyridoxal phosphate.

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CC -!- ENZYME REGULATION: ISOLEUCINE ALLOSTERICALLY INHIBITS WHEREAS
CC VALINE ALLOSTERICALLY ACTIVATES THIS ENZYME.
CC -!- PATHWAY: Isoleucine biosynthesis, first step.
CC -!- SUBUNIT: Homotetramer.
CC -!- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
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CC -----
DB EMBL; M26570; AAA27150.1; -
DB EMBL; AF233324; AA933479.1; -
DB EMBL; AE008862; AAL22755.1; -
DB EMBL; M25498; AAA27151.1; -
DB PIR; J02278; DMBRTT.
DB HSSP; P04968; 1TDJ.
DB StyGene; SG10129; ilvA.
DB InterPro; IPR001926; B6 enzyme_beta.
DB InterPro; IPR000634; S/T dehydratase.
DB InterPro; IPR005787; Thr dehydratase.
DB InterPro; IPR001721; ThrDh_C.
DB Pfam; PF00291; PALP.1.
DB Pfam; PF00585; Thr dehydrat C.2.
DB TIGRFAMs; TIGR01124; ilvA_2Cterm.1.
DB PROSITE; PS00165; DEHYDRATASE_SER_THR.1.
DB KMW Isoleucine biosynthesis; Lyase; Pyridoxal phosphate;
  Allosteric enzyme; Complete proteome.
FT BINDING 62 62 PYRIDOXAL PHOSPHATE.
FT CONFLICT 71 71 A -> T (IN REF. 1).
FT CONFLICT 124 124 F -> L (IN REF. 1).
FT CONFLICT 339 339 A -> G (IN REF. 1).
FT CONFLICT 342 342 A -> T (IN REF. 1).
FT CONFLICT 351 353 SFL -> NFP (IN REF. 1).
SQ SEQUENCE 514 AA; 56253 MW; 136BC35F1F00358 CRC64;

Query Match 95.94; Score 2525; DB 1; Length 514;
Best Local Similarity 95.1%; Pred. No. 2.7e-163;
Matches 489; Conservative 17; Mismatches 8; Indels 0; Gaps 0;

OY 1 MADQPLSGAGEGEYRAVLRAPVTEAQTPLQKMEKSSRLDNLVLYREPROPHS 60
DB 1 MAEQPLSVAGEGAYLAVALRAPVTEAQTPLQKMEKSSRLDNLVLYREBQPVHS 60
OY 61 FKLKGAAYMAGLTBEOKAHGVITASAGNHAQGVAFSSARLGVALLVMPATADIKYDA 120
DB 61 FKLKGAAYMAGLTBEOKAHGVITASAGNHAQGVAFSSARLGVALLVMPATADIKYDA 120
OY 121 VRGEGEVLHGANFDEAKKVAIEISQOQGTWPPDPHVPVINGQTLAELLQODAH 180
DB 121 VRGEGEVLHGANFDEAKKVAIEIAQOQGTWPPDPHVPVINGQTLAELLQODSH 180
OY 181 DRVFPVGGGGLAAGVAVLILKQMLPQIVIAVEADSDACLKAAADAGHPVDLPRVGLFAE 240
DB 181 DRVFPVGGGGLAAGVAVLILKQMLPQIVIAVEADSDACLKAAADAGHPVDLPRVGLFAE 240
OY 241 GVAVKRIDETFRLLCOEYLDDIITVDSDAICAMKDLFEDVRAVAEPGALALAGMKYI 300
DB 241 GVAVKRIDETFRLLCOEYLDDIITVDSDAICAMKDLFEDVRAVAEPGALALAGMKYI 300
OY 301 ALHNHGRRLAHITISGANVNFHGLRYVSEBCELBORFALLAVTIPKSGFLKFCOLLG 360
DB 301 ALHNHGRRLAHITISGANVNFHGLRYVSEBCELBORFALLAVTIPKSGFLKFCOLLG 360
OY 361 GRSVTEFNRYRPAADAKNACIFVGVRLSRGLSEKKEILLQMLNDGYSVDLSDEMAKLVHR 420
DB 361 GRSVTEFNRYRPAADAKNACIFVGVRLSRGLSEKKEILLQMLNDGYSVDLSDEMAKLVHR 420
OY 421 YWVGSRPSHPLQERLYSEFPESPGAKLRFNLTLGTWNISLFHYRSHGTDYGRVLAPE 480
DB 421 YWVGSRPSHPLQERLYSEFPESPGAKLRFNLTLGTWNISLFHYRSHGTDYGRVLAPE 480

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Db      421 YWVGRPSKPLQRLYSFEFEPSPGALLKFLHTLGTWNISLPHYRSHGTDYGRVLAPE 480
QY      481 XGDHEDPFRNLNEIGYDCHDETNNPAFRPFLAG 514
      481 LGDHPDPFRNLNEIGYDCHDETNNPAFRPFLAG 514

RESULT 3
THD1_PASMU STANDARD; PRT; 513 AA.
AC      99CKJ2;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Threonine dehydratase biosynthetic (EC 4.3.1.19) (Threonine
GN      deaminase).
GN      ILVA OR PM1624.
OC      Pasteurella multocida.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC      Pasteurellaceae; Pasteurella.
QX      NCBI_TaxId=747;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Pm70;
RX      MEDLINE=21145866; PubMed=11248100;
RA      May B.J., Zhang O., Li L.L., Paustian M.L., Whitam T.S., Kapur V.;
RT      "Complete genomic sequence of Pasteurella multocida Pm70.";
RL      Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC      -1- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from
CC      threonine in a two-step reaction. The first step is a dehydration
CC      of threonine, followed by rehydration and liberation of ammonia.
CC      -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
CC      -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC      -1- PATHWAY: Isoleucine biosynthesis; first step.
CC      -1- SUBUNIT: Homodimer (By similarity).
CC      -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
CC      -----
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CC      -----
DR      EMBL, AE006199; AK03708.1; -.
DR      HSSP; P04968; ITD.
DR      InterPro; IPR001926; B6_enzyme_beta.
DR      InterPro; IPR000634; S/T_dehydrase.
DR      InterPro; IPR005787; Thr_dehydrater.
DR      InterPro; IPR001721; ThrDh_C.
DR      Pfam; PF00281; PALP; 1.
DR      Pfam; PF00585; Thr_dehydrat_C; 2.
DR      TIGRPFAM; TIGR01124; ilva_2Cterm; 1.
DR      PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
KW      Isoleucine biosynthesis; lyase; Pyridoxal phosphate;
KW      Complete proteome.
FT      BINDING 61
FT      SEQUENCE 513 AA; 56288 MW; 3E427ADC54E5FC7C CRC64;

Query Match      70.5%; Score 1857.5; DB 1; Length 513;
Best local similarity 69.4%; Pred. No. 33e-118;
Matches 352; Conservative 73; Mismatches 79; Indels 3; Gaps 3;

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Db      127 VLLHGANFDEAKAKAIELESKMTFIPFDPHVAIAGGSIAMELLQNSOIDRIFVAV 186
QY      188 GGGGLAAGVAVLIKQMLPOIKYIAVEADPSACLKXALDAGHVLD.PRVGLFEGVAVKRI 247
      187 GGGGLAAGVAVLIKQMLPEIKYIWEESKOSACLYRALKAKPIDDRVGLFADGVAVKRI 246
QY      248 GDETRLCOEYADDIITVDSDAICAMKDLFEDVAVAEVSAGALAGMKYITALHNING 307
      247 GDETRVCCQYITDVLVDGDEICAAVNDIFENVAALIEPSGALISLAGKVKENILOG 306
Db      308 ERLAHLISGANVPHGLRVYSRCELGEORALLAVTIPKSGPLKCOLIGRSVTEP 367
      307 ERLVAVLSGANVPHGLRVYSRCELGEORALLAVTIPKSGPLKCOLIGRSVTEP 366
QY      368 NYRPADAKACIFGVNRLSRGLSEERKEILQWINDGYSVVDLSDDEMAKLHYRVWVGR 427
      367 KYRVADDKACIFGVNRLT-GEERKOTITNOQNGYDILDSNDIATTHVRYMIGRS 425
QY      428 SHPLQRLYSFEFEPSPGAXLRFNLTLG-TYWNISLPHYRSHGTDYGRVLAPEXGDHDP 486
      426 NSPLKERLYSFEFEPKQKALLKFLHTLGTWNISLPHYRSHGTDYGRVLAPEXGDHDP 485
QY      487 D-FETRLNELGYDCHDETNNPAFRPFL 512
      486 DAFNQHLEKLGYYQDVTESPAYRYFL 512

RESULT 4
THD1_HAEIN STANDARD; PRT; 513 AA.
AC      P46453;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Threonine dehydratase biosynthetic (EC 4.3.1.19) (Threonine
GN      deaminase).
GN      ILVA OR HI0738.1.
OC      Haemophilus influenzae.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC      Pasteurellaceae; Haemophilus.
QX      NCBI_TaxId=727;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=RD / KM20 / ATCC 51907;
RX      MEDLINE=95350630; PubMed=7542800;
RA      Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA      Kerevanage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA      McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA      Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA      Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA      Usterback T.R., Hanna M.C., Nguyen D.T., Saudak D.M., Brandon R.C.,
RA      Fine L.D., Fritchman J.L., Fritchman J.L., Geoghagen N.S.M.,
RA      Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA      Venter J.C.;
RT      "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT      Rd.";
RL      Science 269:496-512(1995).
RN      [2]
RP      IDENTIFICATION.
RP      Koonin E.V., Rudd K.E.;
RL      Submitted (SEP-1995) to the SWISS-PROT data bank.
CC      -1- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from
CC      threonine in a two-step reaction. The first step is a dehydration
CC      of threonine, followed by rehydration and liberation of ammonia.
CC      -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
CC      -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC      -1- PATHWAY: Isoleucine biosynthesis; first step.
CC      -1- SUBUNIT: Homodimer (By similarity).
CC      -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
CC      -----
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DR EMBL; U32757; AAC22398.1; -  
 DR HSSP; P04968; 1TDJ.  
 DR TIGR; H10738.1; -  
 DR InterPro; IPR001926; B6\_enzyme\_beta.  
 DR InterPro; IPR000634; S/T\_dehydratase.  
 DR InterPro; IPR005787; Thr\_dehydratase.  
 DR InterPro; IPR001721; ThrDh\_C.  
 DR Pfam; PF00291; PALP; 1.  
 DR Pfam; PF00585; Thr\_dehydratase; 2.  
 DR TIGRfams; TIGR01124; 11vA\_2Cterm; 1.  
 DR PROSITE; PS00165; DEHYDRATASE\_SER\_THR; 1.  
 DR Isoleucine biosynthesis; Lyase; Pyridoxal phosphate;  
 KW Complete proteome.  
 FT BINDING 63  
 SQ SEQUENCE 513 AA; 56662 MW; DF42CA8B6FDE4CD7 CRC64;

Query Match 66.0%; Score 1738.5; DB 1; Length 513;  
 Best Local Similarity 66.7%; Pred. No. 3.6e-110;  
 Matches 337; Conservative 77; Mismatches 86; Indels 5; Gaps 4;

QY 11 PEGAEVRAVLR--APVYEAQVTPLOKMEKLSRLNVLIVKREDQPVHSFLKRGYA 68  
 DB 10 PSQSDYINAIKGSRYVEAAQVTPLOKGLSLRNHNWIKEDRPVNSFLKRGYA 69  
 QY 69 MMAGLTEOKAGVITASAGNHAQVAFSSARLGVKALIVPTADIKVDVAGFGGEV 128  
 DB 70 MISSLSAQKAGVITASAGNHAQVAFSSARLGVKALIVPTADIKVDVAGFGGEV 129  
 QY 129 LHGANEDEAKAKAIEISQOQFTWPPEDHPVIAAGGTALIELLOQDAHLDEVPVVG 188  
 DB 130 LHGANEDEAKAKAIEISQOQFTWPPEDHPVIAAGGTALIELLOQDAHLDEVPVVG 189  
 QY 189 GGGGAAGVAVILKOLMPQIKVIAVEAEDSACLKALADAGHVDLPRVGLFAGVAVRIG 248  
 DB 190 GGGGAAGVAVILKOLMPQIKVIAVEAEDSACLKALADAGHVDLPRVGLFAGVAVRIG 249  
 QY 249 DETFRLCOEYLDITVDSDAICAMKDLFEDVRAVAEPPSAGALAGMKYIALHNIRGE 308  
 DB 250 DETFRLCOEYLDITVDSDAICAMKDLFEDVRAVAEPPSAGALAGMKYIALHNIRGE 309  
 QY 309 RLHHISGANVNFHGLRYVSECEGEORALLAVTIPBEKGSFLKFCOLLGSSVTEFN 368  
 DB 310 RLHHISGANVNFHGLRYVSECEGEORALLAVTIPBEKGSFLKFCOLLGSSVTEFN 369  
 QY 369 YRFADAKACIFVGVRLSRGIEERKEILQMDNGSVVSDDEMAKTLHRYVWVGRRPS 428  
 DB 370 YRFADAKACIFVGVRLSRGIEERKEILQMDNGSVVSDDEMAKTLHRYVWVGRRPS 428  
 QY 429 HPLQERLYSFEPPSPGALRFLNLTIGYWNISLFHYRSHGTDYGRVLAAREXGDHE--PD 487  
 DB 429 ND-NERLYTFEPPSPGALRFLNLTIGYWNISLFHYRSHGTDYGRVLAAREXGDHE--PD 487  
 QY 488 FETRLNELGYDCHDETNNPAFRFL 512  
 DB 488 FETRLNELGYDCHDETNNPAFRFL 512

RESULT 5  
 THD1 BURCE STANDARD; PRT; 507 AA.  
 AC P53607;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Threonine dehydratase biosynthetic (EC 4.3.1.19) (Threonine  
 deaminase).  
 GN ILVA.

OS Burkholderia cephacia (Pseudomonas cepacia).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Burkholderiaceae; Burkholderia.  
 OX NCBI\_TaxId=292;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STEAIN=17616;  
 RA Bartell J.B., Lessie T.G.,  
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from  
 CC threonine in a two-step reaction. The first step is a dehydration  
 CC of threonine, followed by rehydration and liberation of ammonia.  
 CC -1- CATALYTIC ACTIVITY: L-threonine + 2-oxobutanoate + NH(3).  
 CC -1- COFACTOR: Pyridoxal phosphate.  
 CC -1- PATHWAY: Isoleucine biosynthesis; first step.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.  
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DR EMBL; U40630; AA83215.1; -  
 DR HSSP; P04968; 1TDJ.  
 DR InterPro; IPR001926; B6\_enzyme\_beta.  
 DR InterPro; IPR000634; S/T\_dehydratase.  
 DR InterPro; IPR005787; Thr\_dehydratase.  
 DR InterPro; IPR001721; ThrDh\_C.  
 DR Pfam; PF00291; PALP; 1.  
 DR Pfam; PF00585; Thr\_dehydratase; 2.  
 DR TIGRfams; TIGR01124; 11vA\_2Cterm; 1.  
 DR PROSITE; PS00165; DEHYDRATASE\_SER\_THR; 1.  
 DR Isoleucine biosynthesis; Lyase; Pyridoxal phosphate.  
 KW Complete proteome.  
 FT BINDING 52  
 SQ SEQUENCE 507 AA; 55326 MW; E9A5D110B0597664 CRC64;

Query Match 52.5%; Score 1383; DB 1; Length 507;  
 Best Local Similarity 54.1%; Pred. No. 3.6e-86;  
 Matches 273; Conservative 91; Mismatches 133; Indels 8; Gaps 5;

QY 15 EYLRARVRAVYEAQVTPLOKMEKLSRLNVLIVKREDQPVHSFLKRGYAMMGLT 74  
 DB 5 DYLRKILTAIVYDAVFAFTELELPARNISARLRNVPYLLREKNQVPSFLKRGYAMMGLT 74  
 QY 75 EEOKAHGVITASAGNHAQVAFSSARLGVKALIVPTADIKVDVAGFGG--EYLLH 131  
 DB 65 ADALARGVITASAGNHAQVAFSSARLGVKALIVPTADIKVDVAGFGG--EYLLH 131  
 QY 132 GANEDEAKAKAIEISQOQFTWPPEDHPVIAAGGTALIELLOQ-DAHLDEVPVVG 190  
 DB 125 GESYSDAVAAHLKQBERGLTFVHPDDPYVIAAGGTALIELLOQ-DAHLDEVPVVG 190  
 QY 191 GLAAGVAVILKOLMPQIKVIAVEAEDSACLKALADAGHVDLPRVGLFAGVAVRIG 250  
 DB 185 GLAAGVAVILKOLMPQIKVIAVEAEDSACLKALADAGHVDLPRVGLFAGVAVRIG 250  
 QY 251 TFRLOEYLDITVDSDAICAMKDLFEDVRAVAEPPSAGALAGMKYIALHNIRGERL 310  
 DB 245 TFRLOEYLDITVDSDAICAMKDLFEDVRAVAEPPSAGALAGMKYIALHNIRGERL 310  
 QY 311 AHILSGANVNFHGLRYVSECEGEORALLAVTIPBEKGSFLKFCOLLGSSVTEFN 370  
 DB 305 VAATSGANVNFHGLRYVSECEGEORALLAVTIPBEKGSFLKFCOLLGSSVTEFN 370  
 QY 371 PADAKACIFVGVRLSRGIEERKEILQMDNGSVVSDDEMAKTLHRYVWVGRRPS 430  
 DB 365 IADQSHIFVGVQIR-RGESADIANFESHGKTADLHDELSEKIRHYVWVGRRPS 430  
 QY 431 LOERLYSFEPPSPGALRFLNLTIGYWNISLFHYRSHGTDYGRVLAAREXGDHEPD 488

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DB 424 LDERLFRFFPPRPGALMKFLSSMAPDWNLSLFHRNQADVSSILVGLQVQADH-AEF 482
QY 489 ETRNLNELGYDCHDETNNPAFRFLA 513
DB 483 ERFALAGPYVEESANPAYRLFLS 507

RESULT 6
TDH YEAST STANDARD; PRT; 576 AA.
ID THDH YEAST
AC P00927;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DB Threonine dehydratase, mitochondrial precursor (EC 4.3.1.19)
DE (Threonine deaminase).
ILV1 OR YER086W.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Kjelland-Brandt M.C., Holmberg S., Petersen J.G.L.,
RA Nilsson-Tillgren T.;
RT "Nucleotide sequence of the gene for threonine deaminase (ILV1) of
RT Saccharomyces cerevisiae."
RT Carlsberg Res. Commun. 49:567-575 (1984).
RN [2]
RP SEQUENCE FROM N.A.
RA Strain=8288C / AB972;
RC PubMed=9169868 / AB972;
RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
RA Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
RA Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
RA Huntke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
RA Lin D., Moseedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
RA Oh C., Patel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
RA Smith V., Taylor P., Wei Y., Borstein D., Davis R.W.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V."
RT Nature 387:78-81 (1997).
CC -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
CC -1- COFACTOR: Pyridoxal phosphate.
CC -1- ENZYME REGULATION: ISOLEUCINE ALLOSTERICALLY INHIBITS WHILE
CC VALINE ALLOSTERICALLY ACTIVATES THIS ENZYME.
CC -1- PATHWAY: Isoleucine biosynthesis; first step.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
CC
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CC
DR EMBL; M36383; AAA34705.1; -
DR EMBL; X01466; CAA25696.1; -
DR EMBL; U18839; AAB64641.1; -
DR PIR; S50589; DMRYT.
DR HSSP; P04968; ITDU.
DR SGD; S000088; ILV1.
DR InterPro; IPR001926; B6 enzyme beta.
DR InterPro; IPR000634; S/P dehydratase.
DR InterPro; IPR005787; Thr dehydratase.
DR InterPro; IPR001721; Thrdh_C.
DR Pfam; PF00291; PALP; 1.
DR Pfam; PF00585; Thr dehydratase C; 2.
DR TIGRFAMs; TIGR01124; IlvA_2Cterm; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.

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KM Isoleucine biosynthesis; Lyase; Mitochondrion; Pyridoxal phosphate;
KW Transl. peptide; Allosteric enzyme.
FT TRANSIT 1 576 MITOCHONDRION (POTENTIAL).
FT CHAIN ? 576 THREONINE DEHYDRATASE.
FT BINDING 109 109 PYRIDOXAL PHOSPHATE.
FT CONFLICT 259 259 I -> T (IN REF. 1).
SQ SEQUENCE 576 AA; 63831 MW; 0801BCBD7EEDC1F CRC64;

Query Match 46.1%; Score 1212.5; DB 1; Length 576;
Best Local Similarity 47.7%; Pred. No. 1.4e-74;
Matches 247; Conservative 99; Mismatches 147; Indels 25; Gaps 7;

QY 15 EYLRVILAPYEAQVTPPLQMKELSRDLNVILVKEDRQPVHSFRLGAYAMAGLT 74
DB 62 DYRLVLRSSVYDVINESPIQGVCLSRMTNVTNKKEDLLPVSPFLRAGANNIATKD 121
QY 75 EQRKAGVITTSAGNAGVAFSSARLGVKLLIWPFTALIKDANVGFGEVILLHGAN 134
DB 122 DQNRQGVIAQSAGNAGVAFPAKHKLIPATIVPCTPSIKQVSRSLSQVVLGND 181
QY 135 FDEAKAKIELSQOQGFVTPVPPDHPMVIAGQGLALELLQODAHLDL---VFVPVGGGG 191
DB 182 FDEAKAECAKLAERGLTNIPFDHPYVIAQGYAMKILQVRANKIGAVFVPVGGGG 241
QY 192 LAAGVAVILIKOLMPQIKYIAVEAEDSACKALADGHPVDLPVGLFAEGVAVKRIQDET 251
DB 242 LIAGGAVLKVAAPHIKILIGVETVDAATLHNSLQNRQTPLPVVGTFADGTSVEMIGET 301
QY 252 FRLCEYLDITITVDSALICAMKDLFEDVAVAVAPSSGALLAGKKYITA-LHNIRGRL 310
DB 302 FRVAQVVDDEVVLVNTDEICAAVNDIFEDTSSIVPSGALSVAGKKYISTVH---DEI 357
QY 311 AH-----ILSGAVNFGHLYVSERCLEGEORFALLAVTIPEKSGFLKCOLLAGRS 363
DB 358 DHTKATYVPIISGANMNDRLRFVSEKAVLDEGEVFMVTLPLDVGAFKMGQKIHPRS 417
QY 364 VTEFNRYR-----ADAKNACIFVGVRLSGLEERKEILQMLNDGYSVVDLSDDEMA 415
DB 418 VTEFSRYNHRHESSSVPRAYITVSFVVDREKEIKQWQQLNALFEAVDLSIDNELA 477
QY 416 KLVHRYMVGSRPHQLQRLYSFEPSPGAXLRPLNTLGTWNLSLHYHSHGDXRY 475
DB 478 KSHGYYLVGASQVY-NRRIISFEPPERGALTRFLGGLSSWNLTLPHRYNHGADIGRY 536
QY 476 LAAPFGDHP--DEPTRLNELGYDCHDETNNPAFRFL 512
DB 537 LAGISVPRENLTPOKFLIEDLGYTHDETDTVIVQKL 574

RESULT 7
TDH ARXAD STANDARD; PRT; 550 AA.
ID THDH ARXAD
AC O42615;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Threonine dehydratase, mitochondrial precursor (EC 4.3.1.19)
DE (Threonine deaminase).
ILV1.
OS Arxula adeninivorans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; mitosporic Dipodascaceae; Arxula.
OX NCBI_TaxID=37620;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=LS3;
RC MEDLINE=98398049; PubMed=9730281;
RA Wartmann T., Roedel H., Kunze I., Bode R., Kunze G.;
RT "Ilv1 gene from the yeast Arxula adeninivorans LS3 -- a new selective
RT transformation marker."
RT Yeast 14:1017-1025 (1998).
CC -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
CC -1- COFACTOR: Pyridoxal phosphate.

```

CC -1- PATHWAY: Isoleucine biosynthesis; first step.  
 CC -1- SUBUNIT: Homotetramer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.  
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 CC  
 DR EMBL: AJ222772; CAA10977.1; .  
 DR HSSP: P04968; ITDJ.  
 DR InterPro: IPR001926; B6 enzyme beta.  
 DR InterPro: IPR000634; S/T\_dehydratase.  
 DR InterPro: IPR005787; Thr\_dehydratase.  
 DR InterPro: IPR001721; ThrDh\_C.  
 DR Pfam: PF00291; PALP; 1.  
 DR Pfam: PF00585; Thr\_dehydratase; 2.  
 DR TIGRfam: TIGR01124; tlyA-2Cterm; 1.  
 DR PROSITE: PS00165; DEHYDRATASE\_SER\_THR; 1.  
 DR Isoleucine biosynthesis; Lyase; Mitochondrion; Pyridoxal phosphate;  
 KM Transient peptide.  
 FT TRANSIT 1 ? MITOCHONDRION (POTENTIAL).  
 FT CHAIN ? 550 THREONINE DEHYDRATASE.  
 FT BINDING 86 86 PYRIDOXAL PHOSPHATE.  
 FT SEQUENCE 550 AA; 6046 MW; D08CE5B55CC8A6F CRC64;  
 SQ  
 Query March 43.1%; Score 1136; DB 1; Length 550;  
 Best Local Similarity 45.2%; Pred. No. 1.9e-69;  
 Matches 236; Conservative 98; Mismatches 164; Indels 24; Gaps 9;  
 QY 11 PEGA-EYLRAVLAPEAAYVTPAQKMEKLSRLDNLVLRKEDROPVHFKLGAAYAM 69  
 DB 34 PDGTPDYKILKLSKVVDVCEIETPTPAVNLSSKLGANIFLKRBDLPVSEFKLRGAYNM 93  
 QY 70 MAGITEQKXAGVTTASAGNHAQVAFSASALGVKALIMPTARADIKNDAVRFGEVYL 129  
 DB 94 MAHLPQSTRKMGVAGSAGNHAQVAFSASALGVKALIMPTARADIKNDAVRFGEVYL 153  
 QY 130 LHGANPEAKAKAIELEQQOQFTWVPFDPHVPVAGGTTALDELQOQ-DAH-IDRVFVVP 187  
 DB 154 LHGNDFPAARAEKCRLEKRGITNIPFDNPYVYAGGTTGVELLRQIDVESLAIIVCI 213  
 QY 188 GGGGLAAGVAVLIRQLMPQIKVIAVEADSAKLKALDAGHPVDLPRVGLPAEGVAVKRI 247  
 DB 214 GGGGLIAGVAVYKRIAPQYKIIIGETVDANAMQSLQKGBRITLSEVGLFADGAAYKIL 273  
 QY 248 GDEFFRLCOEYLDITIVDSALTCAMKDLFEDVRAVAEBSGALALAGMKYTLAHNRG 307  
 DB 274 GEEFFRLCOQVVDIVSTDEIQAIAKDVTEFRSLIVEPAGALSVAGLVYVESH- 329  
 QY 308 ERLAH-----LISGANVNFHGRVYSERCELEGEDEALLAVTIPERKSGFLFCOLLG 360  
 DB 330 PEITHSASGTRAILISGANMDRLRFVSEKAKLEGESEVFVATIPERKSGFGALIDLVAH 389  
 QY 361 GRASVTEFNYPADAK-----NACIFGVRLSRGLSEERKEILLQMLNDGQSVVDLSDDEM 414  
 DB 390 PRAVTEFSYRSNGELEKSDGKAHAYISFSDVNAKAEVPRILDDFKAGGFAIDISHNEF 449  
 QY 415 AKLHVRVWNGRBPBHL-QERLYSFFPPESGALIRPLNTLIGTWNISLFFYRSHGVDYG 473  
 DB 450 PKSHPRYLVA-NQPTVNERVFRPEPERGALVKFLHAGKSKWNTTLFHYRQSGDIA 507  
 QY 474 RVLAPEKXGHEPD-FETRLNELGVDGDETNNPAPFPFLAG 514  
 DB 508 KVLVAGISVPSHESDQFQFLDNLVRYAEEDNVVYKLFSGG 549

ID THD1\_ARATH STANDARD; PRT; 592 AA.  
 AC Q9ZS6; Q9SPF1;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Threonine dehydratase biosynthetic, chloroplast precursor  
 DE (BC 4.3.1.19) (Threonine deaminase) (TD).  
 GN OMRI OR AT3G10050 OR T22K18.12.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; Rosidae;  
 OC euroside II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Mourad G., Emerick R., Marion A., Smith A.;  
 RT "Cloning and sequencing of a cDNA encoding threonine dehydratase/  
 RT deaminase of Arabidopsis thaliana.";  
 RL (in) Plant Gene Register PGR98-199.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Mourad G.S., Smith A.M.;  
 RT "Molecular characterization of the genomic clone, including the  
 RT promoter sequences, of threonine dehydratase/deaminase from  
 RT Arabidopsis thaliana.";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. GMI1b;  
 RX MEDLINE=20144028; PubMed=10677454;  
 RA Mourad G., Emerick R., Smith A.;  
 RT "Molecular cloning and sequencing of a cDNA encoding an isoleucine  
 RT feedback insensitive threonine dehydratase/deaminase of Arabidopsis  
 RT thaliana line GMI1b.";  
 RL (in) Plant Gene Register PGR00-020.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016720; PubMed=11130713;  
 RA Salanoubat M., Lemcke K., Rieger M., Perez-Alonso M., Obermaier B.,  
 RA Fatmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,  
 RA Delaney M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,  
 RA De Simone V., Choisy N., Artiguenave F., Robert C., Brotier P.,  
 RA Wincker P., Catolico L., Weissenbach J., Saurin W., Querrier F.,  
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs W., Benes V.,  
 RA Wirmelmann E., Dizonak H., Erlie H., Jordan N., Bangert S.,  
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,  
 RA Verzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,  
 RA Conrad A., Hornischer K., Kauer G., Loehart T.-H., Nordstiek G.,  
 RA Reichelt J., Scharte M., Schoen O., Bargues M., Terol J., Clement J.,  
 RA Navarro P., Collado C., Perez-Perez A., Oudemaelde B., Duchemin D.,  
 RA Cooke R., Landie M., Berger-Delaurio C., Fumelle B., Masny D.,  
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottelet A., Casacuberta E.,  
 RA Monfort A., Argüeso A., Flores M., Ligouri R., Vitale D.,  
 RA Mannheim J., Haase D., Schoof H., Rudi S., Zaccaria P., Mewes H.-W.,  
 RA Meyer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,  
 RA Rooney T., Rizzo W., Walts A., Ulteback T., Fujii C.Y., Shea T.P.,  
 RA Creasy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,  
 RA Pai G., Miltischer J., Sellers P., Gill J.E., Feldlyum T.V.,  
 RA Preuss D., Lin X., Nieman W.C., Salzberg S.L., White O., Venter J.C.,  
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asanizu E.,  
 RA Sasamoto S., Kimura T., Ideawara K., Kawashima K., Kishida Y.,  
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,  
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;  
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis  
 RT thaliana.";  
 RL Nature 408:820-822(2000).  
 CC -1- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from  
 CC of threonine in a two-step reaction. The first step is a dehydration  
 CC of threonine, followed by rehydration and liberation of ammonia.  
 CC -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).

RESULT 8  
 THD1\_ARATH



CC -1- COPACITOR: Pyridoxal phosphate (By similarity).  
 CC -1- ENZYME REGULATION: Allosterically inhibited by isoleucine. Strain  
 CC antimetabolite L-O-methylthreonine.  
 CC -1- PATHWAY: Isoleucine biosynthesis; first step.  
 CC -1- SUBCELLULAR LOCATION: Chloroplast (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.  
 CC -----  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL, AF096281; AAC97936.1; -  
 CC EMBL, AF221984; AAF32370.1; -  
 CC EMBL, AF177212; AAD54324.1; -  
 CC EMBL, AC010927; AAF04418.1; -  
 CC PIR, T51712; T51712.  
 CC HSP, P04968; ITD.  
 CC InterPro: IPR001926; B6 enzyme beta.  
 CC InterPro: IPR000634; S/T dehydratase.  
 CC InterPro: IPR005787; Tht dehydratet.  
 CC InterPro: IPR001721; Thrdh\_C.  
 CC Pfam: PF00291; PALP; 1.  
 CC Pfam: PF00585; Tht\_dehydrat\_C; 2.  
 CC TIGRfam: TIGR01124; IIVA\_2cterm; 1.  
 CC PROSITE, PS00165; DEHYDRATASE SER THR; 1.  
 CC Isoleucine biosynthesis; lyase; Chloroplast; Pyridoxal phosphate;  
 CC Allosteric enzyme; Transit peptide.  
 FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).  
 FT CHAIN 1 592 THREONINE DEHYDRATASE BIOSYNTHETIC.  
 FT BINDING 141 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 FT VARIANT 499 R -> C (IN STRAIN GML1B).  
 FT VARIANT 544 R -> H (IN STRAIN GML1B).  
 SO SEQUENCE 592 AA; 64634 MW; 16658747052FAE7C CRC64;

Query Match 41.3%; Score 1087; DB 1; Length 592;  
 Best Local Similarity 44.5%; Pred. No. 4.3e-66;  
 Matches 226; Conservative 101; Mismatches 167; Indels 14; Gaps 6;

QY 12 EGAEYLRARVRAVYEAQVTPLOQKMKSSRLDNVILVREPROVHSFKLGGAYAMA 71  
 DB 91 EANEYLTNLTSTKVYIAIESPQLAKKSKRLGVRYLGRBDLQVSEFKLGGAYAMV 150  
 QY 72 GLTEBOKAGVITASAGNHQGVAFSSARLGVKALLVMPATADIKVDVRFGEVLLH 131  
 DB 151 KLRADQLAGVITSSAGNHQGVAFSSARLGVKALLVMPATADIKVDVRFGEVLLH 210  
 QY 132 GANFDEAKAKATLSQOQGFVTPPDHNVINGOGTALALILQ-DAHLDRVFPVGG 190  
 DB 211 GDSYDOAQAARAKIRAESEGLTFPPDPHNVINGOGTALALILQ-DAHLDRVFPVGG 270  
 QY 191 GLAAGVAVLKQMLPQIKVAVAEASACIKALDGHPRDLPRVGLAEVAVKRGISE 250  
 DB 271 GLTAGLAAYVRRVSPVKIIGVPRADANANALSLHGERYLDQVGAFADGAVAVKRGISE 330  
 QY 251 TFLICEYLDLITVSDAICAMKDLFEDVRAVAPSGALALAKMKYITALINIGRL 310  
 DB 331 TFLISRLMDGVVLTTRDAICAIKQMEFKRIILBPAGLALALAGAEVAKYGLDVMV 390  
 QY 311 AHLISGANVFFGLRVYSERCGEORALLAVTPEKGSPLKFCOLLGSRVTEPNR 370  
 DB 391 VAITSANNNFDFKRIYTELAVNGROEAVLATIMEKPSFKOFCELVPMNISSEFKYR 450  
 QY 371 PADAKAACIF--VGNLS---RGLERKELTQMLNDGSGYVNDLSDDEMAKLVHVMWG 425  
 DB 451 CSSEKRAVAVLYSGVHTAGELKALQKMESSQL-----KTVNLVTSDLVKDLRLYMG 504  
 QY 426 RPHPLQERLYSEFPSPGAXRFLNTLTGYNNISLFHRSRGDTGRLTALAEKGDH 485

DB 505 R-STVGEVLGRFPPERPGALMNFDSFSPRNITLFHYRGQGTGANLVGQVPEOE 563  
 QY 486 -PDFETRLNEGYCHDETNNPAPRFL 512  
 DB 564 MEERNNRAKALGYDFLVSDDYFKLM 591

RESULT 9  
 ID THD1\_LYCSES STANDARD; PRT; 595 AA.  
 AC P25306;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Threonine dehydratase biosynthetic, chloroplast precursor  
 DE (EC 4.3.1.19) (Threonine deaminase) (TD).  
 GN TD.  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4081;  
 RN (1)  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 52-61.  
 RC STRAIN=CV. TINY TIM LA154;  
 RX MEDLINE=9118785; PubMed=2011578;  
 RA Samach A., Hareven D., Gutfinger T., Ken-Dror S., Lifschitz E.;  
 RT "Biosynthetic threonine deaminase gene of tomato: isolation,  
 RT structure, and upregulation in floral organs".  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2678-2682(1991).  
 CC -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).  
 CC -1- COPACITOR: Pyridoxal phosphate.  
 CC -1- ENZYME REGULATION: ALLOSTERICALLY INHIBITED BY ISOLEUCINE.  
 CC -1- PATHWAY: Isoleucine biosynthesis; first step.  
 CC -1- SUBUNIT: Homotetramer.  
 CC -1- SUBCELLULAR LOCATION: Chloroplast.  
 CC -1- MISCELLANEOUS: EXPRESSION IN MATURE FLOWERS IS INCREASED OVER  
 CC 500-FOLD.  
 CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL, M61914; AAA34171.1; -  
 CC EMBL, M61915; AAA68097.1; -  
 CC PIR, A38628; A38628.  
 CC HSP, P04968; ITD.  
 CC InterPro: IPR001926; B6 enzyme beta.  
 CC InterPro: IPR000634; S/T dehydratase.  
 CC InterPro: IPR005787; Tht dehydratet.  
 CC InterPro: IPR001721; Thrdh\_C.  
 CC Pfam: PF00291; PALP; 1.  
 CC Pfam: PF00585; Tht\_dehydrat\_C; 2.  
 CC TIGRfam: TIGR01124; IIVA\_2cterm; 1.  
 CC PROSITE, PS00165; DEHYDRATASE SER THR; 1.  
 CC Isoleucine biosynthesis; lyase; Chloroplast; Pyridoxal phosphate;  
 CC Allosteric enzyme; Transit peptide.  
 FT TRANSIT 1 51 CHLOROPLAST.  
 FT CHAIN 1 595 THREONINE DEHYDRATASE BIOSYNTHETIC.  
 FT BINDING 143 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 SO SEQUENCE 595 AA; 64937 MW; AC430B5DD9F0348 CRC64;

Query Match 37.8%; Score 994.5; DB 1; Length 595;  
 Best Local Similarity 41.8%; Pred. No. 7.7e-60;  
 Matches 215; Conservative 100; Mismatches 192; Indels 7; Gaps 6;

QY 4 SLPGLS-AEGAEYLRARVRAVYEAQVTPLOQKMKSSRLDNVILVREPROVHSFK 62



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Db      84 NKPTGSDDELFOYVVDILASFPVDVAIESPLELEKLSDRIGVNFYIKREDKQRFVSPK 143
Qy      63 LRGAYAMMAGLTREOKAHGVITASAGNHAQGVAFSSARLGVKALIVMPTATADIKVDAVR 122
Db      144 LRGATNMNSNLSREELDKGVITASAGNHAQGVALLAGQNLCAKIVMTPTTTPQIKIDAVR 203
Qy      123 GFGGVEVLHGANFDEAKAKAIELSQOQGFVWPPFDHPMVIVAGGTLALBELLOQDAHLDR 182
Db      204 ALGGDVLYXGKTFDEAQTHALELSKDGKIKYIPFDDPGVIVKGQGTIGTEINRQDKDIAH 263
Qy      183 VFPVPGGGGLAGVAVLIKQMLPQIKVAVAEABDSACLKALDAGHPVDLPVGVFAAGV 242
Db      264 VFIPVGGGGLAGVATFFKQIALPNKIKIGVEPYGASMTLSHEHRVYKLSNVDPFAAGV 323
Qy      243 AVKRGDETFPLCQYLDIITVDSDAICAAKMDLFEDVRAVAEBSGALALAGMKKYIAL 302
Db      324 AVALVGETTFACQQLIDGMVIVANDGISAAIKDYDEGRNILETSGAVAIAGAAYCEP 383
Qy      303 HNIRGERLAHLISGANVNFHGLRYVSECEGEORBALLAVTIPEKGSFLKFCOLLGGR 362
Db      384 YKIKENIVAIASGANMDFSKLHKVTELGLSGKREALLATFPMVQGSFKTFVGLVGS 443
Qy      363 SVTEFNRYF-ADAKNACIFVGRVLSRGLEERKEIIOMLNDGYSVVDLSDDEMAKLHRY 421
Db      444 NFTLTYFTSERKXALILRYNVNDEK-SDEKMIEDKSSNMNTLNSHELVDHLKH 502
Qy      422 MYGGRPSHPLQERLY-SFEFPESPGAXLRFINTLTGYNNISLFHYRSHGTDYGRVLAPE 480
Db      503 LVGG--SANISPEIGEFIVPEKATLKTFLDAPSPRNMTITLCRRNOGDINASILMGPQ 560
Qy      481 XGDHEPD-FETRLNELGYDCHDETNNPAFRFELA 513
Db      561 VPQAEEMDEFKQADKLGYPYELDNVNEAFNLVVS 594

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## RESULT 10

```

THD1_CICAR      STANDARD;      PRT;      590 AA.
ID              AC
AC      039469;
HDT      28-FEB-2003 (Rel. 41, Last sequence update)
HDT      28-FEB-2003 (Rel. 41, Last sequence update)
DRT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Threonine dehydratase biosynthetic, chloroplast precursor
DE      (EC 4.3.1.19) (Threonine deaminase) (TD).
OS      Cicer arietinum (Chickpea) (Garbanzo).
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eustosids I; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.
OX      NCBI_TaxId=3827;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CV. PUSA 261 / PCITD 2, TISSUE=Seed;
RX      MEDLINE=95232188; PubMed=7716234;
RA      John S.J., Srivastava V., Guha-Mukherjee S.;
RT      "Cloning and sequencing of chickpea cDNA coding for threonine
RT      deaminase.";
RL      Plant Physiol. 107:1023-1024 (1995).
CC      -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
CC      -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC      -1- ENZYME REGULATION: ALLOSTERICALLY INHIBITED BY ISOLEUCINE (By
CC      similarity).
CC      -1- PATHWAY: Isoleucine biosynthesis; first step.
CC      -1- SUBCELLULAR LOCATION: Chloroplast (By similarity).
CC      -1- TISSUE SPECIFICITY: FOUND AT HIGHER LEVELS IN FLOWERS THAN IN
CC      OTHER ORGANS.
CC      -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/

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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: X78575; CAAS5313.1; -.
DR      PIR: T09532; T09532.
DR      HSSP: P04968; 1TDJ.
DR      InterPro: IPR001926; B6 enzyme_beta.
DR      InterPro: IPR000634; S/T dehydratase.
DR      InterPro: IPR005787; Thr dehydratase.
DR      InterPro: IPR001721; ThrDh_C.
DR      Pfam: PF00291; PALP; 1.
DR      Pfam: PF00585; Thr dehydrat C; 2.
DR      TIGRFAMs: TIGR01124; liva_2Cterm; 1.
DR      PROSITE: PS00165; DEHYDRATASE_SER_THR; FALSE NEG.
KW      Isoleucine biosynthesis; Lyase; Chloroplast; Pyridoxal phosphate;
KW      Allosteric enzyme; Transil peptide.
FT      TRANSIT      1      44      CHLOROPLAST (POTENTIAL).
FT      CHAIN      45      590      THREONINE DEHYDRATASE BIOSYNTHETIC.
FT      BINDING      139      139      PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ      SEQUENCE      590 AA; 65153 MW; 01D7736AC92BCDEA CRC64;

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Query Match      35.6%; Score 937.5; DB 1; Length 590;
Best Local Similarity      41.5%; Pred. No. 5,4e-56;
Matches      216; Conservative      92; Mismatches      178; Indels      35; Gaps      12;

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Qy      2 ADSQPLSGAPGAEYLRVAVRPAVYEAQVTPLOKMEKLSRLDNVILVKREDROPVHSF 61
Db      85 ADSDEL-----PEYLRLDVASLPYDVDESPEVLETERLSDRLGVNFVKREDRQRFVSF 138
Qy      62 KLRGAYAMMAGLTREOKAHGVITTSAGNHAQGV--ASSARLGVKALIVMPTATADIKV 119
Db      139 KLRGAYAMMAGLTREOKAHGVITTSAGNHAQGV--ASSARLGVKALIVMPTATADIKV 198
Qy      120 AVRGGEVFLHGANFDEAKAKATELSQOQGFVWPPFDHPMVIVAGGTLALBELLOQDAH 179
Db      199 GVRALGADVLMGTFDEAKTHAVELCKDGLRTITPEEDPAVTKGQGTIGTEINRQDKR 258
Qy      180 LDRVFPVPGGGGLAGVAVLIKQMLPQIKVAVAEABDSACLKALDAGHPVDLPVGVFA 239
Db      259 IDAVFVPVGGGGLAGVAVFAFKQIALPQIKIIVPEPYDAASVALSVHHRAKLSNVDPFA 318
Qy      240 EGVAVKRIQDETFFLCQYLDIITVDSDAICAAKMDLFEDVRAVAEBSGALALAGMKKY 299
Db      319 DGATVAVGTEYTFARCDVDVAMVLVANDGIGAAIKDFDEGRNIVERTSGAAGIAGM--Y 376
Qy      300 IALNIRGERLAHLISGANVNFHGLRYVSECEGEORBALLAVTIPEKGSFLKFCOLL 359
Db      377 CEMTRIKNDNMNVGVSGANMNFRLHKVSELAVALGSGHEALLGYTTPQKCCFTMAGLV 436
Qy      360 -GGRSVTEFNRYFADAKNACIFVGRVLS--RGLEERKEIIOMLNDGYSVVDLSDDEMAK 416
Db      437 HGSLSFTEITRYTRFSHRSLIVMLKLEPRKTYI--KMIEMKYSGVTVINISHNELAV 493
Qy      417 LHVRYMVGGRPSHPLQERLY-SFEFPESPGAXL-RFINTLTGYNNISLFHYRSHGTDYGR 474
Db      494 IHGKHLVGG--SAKVSDEVFEFIIPEK--ADLKKEFLEIVSPHNMLTLRYRNOGDILKAT 549
Qy      475 VLAAPFKGDHEPD-----ETRLNELGYDCHDETNNPAFRFELA 508
Db      550 ILMYIAS-----FLCEIVIRKNOIDIGYPYEIDQYNDAF 584

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## RESULT 11

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THD1_SOLTU      STANDARD;      PRT;      359 AA.
ID              AC
AC      P31212;
HDT      01-JUL-1993 (Rel. 26, Created)
HDT      01-JUL-1993 (Rel. 26, Last sequence update)
DRT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Threonine dehydratase biosynthetic (EC 4.3.1.19) (Threonine deaminase)
DE      (TD) (Fragment).
GN      TD.
OS      Solanum tuberosum (Potato).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC  Asteridae; lamiales; Solanales; Solanaceae; Solanum.
OX  NCBI_TaxID=4113;
RN  (1)
RP  SEQUENCE FROM N.A.
RC  STRAIN=cv. Desiree; TISSUE=leaf;
RX  MEDLINE=93005746; PubMed=1392612;
RA  Hildmann T., Ebneth M., Pena-Cortes H., Sanchez-Serrano J.J.,
RA  Willnitzer L., Prat S.;
RA  "General roles of abscisic and jasmonic acids in gene activation as a
RA  result of mechanical wounding.";
RT  Plant Cell 4:1157-1170(1992).
CC  -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
CC  -1- COFACTOR: Pyridoxal phosphate.
CC  -1- ENZYME REGULATION: ALLOSTERICALLY INHIBITED BY ISOLEUCINE.
CC  -1- PATHWAY: Isoleucine biosynthesis; first step.
CC  -1- SUBUNIT: Homotetramer.
CC  -1- SUBCELLULAR LOCATION: Chloroplast.
CC  -1- TISSUE SPECIFICITY: FLORAL BUDS OF UNTREATED PLANTS. AFTER ABA
CC  TREATMENT OR MECHANICAL WOUNDING IS MOSTLY ACCUMULATED IN LEAVES,
CC  TO A LESSER EXTENT IN STEMS, BUT NOT IN ROOTS.
CC  -1- INDUCTION: BY ABSICISIC ACID (ABA), JASMONIC ACID (JA) AND
CC  WOUNDING.
CC  -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X67846; CAA48039.1; -.
DR  PIR; P00468; P00468.
DR  HSSP; P04968; 1TDJ.
DR  InterPro; IPR001926; B6 enzyme beta.
DR  InterPro; IPR000634; S/T dehydratase.
DR  InterPro; IPR001721; ThrdD_C.
DR  Pfam; PF00291; PALP; 1.
DR  Pfam; PF00585; Thr dehydratase C; 2.
DR  PROSITE; PS00165; DEHYDRATASE SER THR, PARTIAL.
KW  Isoleucine biosynthesis; lyase; chloroplast; pyridoxal phosphate;
KW  Allosteric enzyme.
FT  NON_TER
FT  SEQUENCE
SQ  359 AA; 39088 MW; 94DC75974AF9EA30 CRC64;
X  Query Match 24.4%; Score 642; DB 1; Length 359;
X  Best Local Similarity 38.8%; Pred. No. 2,6e-36;
Matches 140; Conservative 68; Mismatches 147; Indels 6; Gaps 5;
QY 156 PEDHPNVIAGQGLTLELLQODAHDRVPVVGSGGLAGVAVLTIQLMPOIVIAVEAE 215
DB 1 PEDAPVVIKGGGTIGTEINRQLKDIAHAFVPPVGGGIGSVAVFYQVAPHTKIGVEPY 60
QY 216 DSGCLAAADAGRPVLLPRVGLFAGGVAVYKIDDERFRLCOEVLDDIITVDSALCAAMK 275
DB 61 GAASMTLSLYEGHRAVLENDVTFADGVAALVGEYTFACQELIDENVLFRNGISAPAK 120
QY 276 DLEEDRAVAAPSGALALAGMKRYIALHNIRGRILHILSGAVNPHGLRYVESECELS 335
DB 121 DVADEGRNIIETSGAVAIAGAAAYCEFYNNKNNIYAIASGAMDSKLKHTLAEELS 180
QY 336 QREBALLAVTTPEEKSGFLKCOLLGGRSVTEFYRP-ADAKNAICIFVGRVLSGLEERKE 394
DB 181 DNEALLATFMIEQGSEFKTFPAKLVGSMNITEVTYRFTSEKELVLYRVDDVDE-KSDLRE 239
QY 395 ILQMLNDGGSVVDLSDDEMAKLVHYMVGGRSPHLOEELY-SFEPPEPQKXLAFLNT 453
DB 240 MIRKLNSNNKTFNFHSHNELVAEHIRKLVGSGAS--ISDEIFGEFIFPEKAGTLSTFLER 297
QY 454 LGTYNNISLPHYRSHGTDYGRVLAFAEXGDHPD-PETRLNELGYCHDETNNPAPRFFL 512

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DB 298 FSPRNNITLCRYRDQDINGNVLVGFQVPOSEHMEFKSQADGLGYPYELDMSNEAFNIVV 357
QY 513 A 513
DB 358 A 358
RESULT 12
THD1_BACSU STANDARD; PRT; 422 AA.
AC P37946;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Threonine dehydratase biosynthetic (Ec 4.3.1.19) (Threonine
DE deaminase).
GN ILVA.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RL Submitted (xxx-1991) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / Maiburg;
RX MEDLINE=96349105; PubMed=8760912;
RA Sorokin A.V., Azevedo V., Zumbstein E., Galleron N., Ehrlich S.D.,
RA Serror P.;
RT "Sequence analysis of the Bacillus subtilis chromosome region between
RT the serX and kds loci cloned in a yeast artificial chromosome.";
RL Microbiology 142:2005-2016(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kuner F., Ogasawara N., Moszer I., Albertini A.M., Allion G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillette R., Boursier L., Brans A., Braun M., Brignall S.C., Bron S.,
RA Brouillette S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Comercon I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Davine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Halech U., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapdue A., Lardinois S., Lauret J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Puje P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeder R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Serror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Taccouti B., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpersa P., Tognoni A.,
RA Tosato V., Uchiyama S., Vanderbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weizengger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis ";
RL Nature 390:249-256(1997).
CC -1- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from
CC threonine in a two-step reaction. The first step is a dehydration
CC of threonine, followed by rehydration and liberation of ammonia.
CC -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).

```

CC -1- COFACTOR: Pyridoxal phosphate.  
 CC -1- PATHWAY: Isoleucine biosynthesis: first step.  
 CC -1- SIMILARITY: BELONGS TO THE SERINE/TREONINE DEHYDRATASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M58606; AAA2549.1; -  
 DR EMBL: L77246; AAA96639.1; -  
 DR EMBL: Z99115; CAB14095.1; -  
 DR PIR: A69644; A69644.  
 DR HSSP: P04968; 1TDJ.  
 DR Subtilist; BG10673; 11VA.  
 DR InterPro: IPR001926; B6 enzyme beta.  
 DR InterPro: IPR000634; S/T dehydratase.  
 DR InterPro: IPR001721; Thrdh\_C.  
 DR Pfam: PF00291; PALP; 1.  
 DR Pfam: PF00585; Thr dehydrat\_C; 1.  
 DR PROSITE: PS00165; DEHYDRATASE\_SER\_THR; 1.  
 KW Isoleucine biosynthesis; Lyase; Pyridoxal phosphate;  
 KW Complete proteome.  
 FT BINDING 60 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 FT CONFLICT 15 15 H -> D (IN REF. 2).  
 FT CONFLICT 139 139 V -> A (IN REF. 2).  
 FT SEQUENCE 422 AA; 46701 MW; 3027A5ED87084140 CRC64;  
 SQ  
 Query Match 24.4%; Score 642; DB 1; Length 422;  
 Best Local Similarity 38.3%; Pred. No. 3.2e-36;  
 Matches 149; Conservative 74; Mismatches 136; Indels 10; Gaps 7;  
 QY 32 TPLQKMEKLSRLDNVILVKREDROPVHSFKRGAYMMAGLTEEOKAHGVITASAGNHA 91  
 DB 30 TPLQKMEKLSRLDNVILVKREDROPVHSFKRGAYMMAGLTEEOKAHGVITASAGNHA 89  
 QY 92 QGVAFSSARLVKALIVMPTATADIKVDVAFRGG--EVLHGANDPEAKAKIELSQ 148  
 DB 90 QGVAFSSARLVKALIVMPTATADIKVDVAFRGG--EVLHGANDPEAKAKIELSQ 149  
 QY 149 QGFTWVPFPHMPTVIAQGGTALAELOQ-DAHMDRVNVPVGGGGLAGAVNLKQMLPQI 207  
 DB 150 ESRFTHFDDPDVWAGGTLAVELINDITREHFLFASVGGGLSGVGYTLKNVSPDT 209  
 QY 208 KVIAVEADSACLAALDAGHPVDLPVGLFAEGVAVKRIQDETFRLCOEYLDIDITVDS 267  
 DB 210 KVIAVEADSACLAALDAGHPVDLPVGLFAEGVAVKRIQDETFRLCOEYLDIDITVDS 269  
 QY 268 DATCAAMKDLFEDVRAVAEBSGALALAGMKKYIALHNIRGERLAHLISGANVNFHGLRV 327  
 DB 270 GKVCTSIETELNECAVVAEPAGALSVALLDLY--KDQIKGNVVCVSGGNNDIGRQEM 327  
 QY 328 SERELGEQRALLAVITPEKSGFLKFC-QLLG-GNSVTEFNFRPADK-NACIFGVGR 384  
 DB 328 KERLIIEGLOHYITVNPQAGALREFLDVLPNDITREYTKKNNKSGNPGALVGE 387  
 QY 385 LSRGLEERKEILLQMLNDGYSVVDLSDE 413  
 DB 388 L-QMKADYGLIERMNNKKPHRYVEVKNDE 415  
 RESULT 13  
 THD1\_BACHD STANDARD; PRT; 415 AA.  
 AC O9K663;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Threonine dehydratase biosynthetic (EC 4.3.1.19) (Threonine  
 deaminase).

GN ILVA OR BH1711.  
 OS Bacillus halodurans.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=6665;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C-125 / JCM 9153;  
 RX MEDLINE=20512582; PubMed=11058132;  
 RA Takaki H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
 RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,  
 RA Horikoshi K.;  
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
 RT halodurans and genomic sequence comparison with Bacillus subtilis";  
 RL Nucleic Acids Res. 28:4317-4331(2000).  
 CC -1- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from  
 CC threonine in a two-step reaction. The first step is a dehydration  
 CC of threonine, followed by rehydration and liberation of ammonia.  
 CC -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).  
 CC -1- COFACTOR: Pyridoxal phosphate.  
 CC -1- PATHWAY: Isoleucine biosynthesis: first step.  
 CC -1- SIMILARITY: BELONGS TO THE SERINE/TREONINE DEHYDRATASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AP001512; BAB05430.1; -  
 DR PIR: G83863; G83863.  
 DR HSSP: P04968; 1TDJ.  
 DR InterPro: IPR001926; B6 enzyme beta.  
 DR InterPro: IPR000634; S/T dehydratase.  
 DR InterPro: IPR001721; Thrdh\_C.  
 DR Pfam: PF00291; PALP; 1.  
 DR Pfam: PF00585; Thr dehydrat\_C; 1.  
 DR PROSITE: PS00165; DEHYDRATASE\_SER\_THR; 1.  
 KW Isoleucine biosynthesis; Lyase; Pyridoxal phosphate;  
 KW Complete proteome.  
 FT BINDING 53 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 FT SEQUENCE 415 AA; 46469 MW; BF49D28B65C7CF2A CRC64;  
 SQ  
 Query Match 23.1%; Score 608; DB 1; Length 415;  
 Best Local Similarity 34.7%; Pred. No. 6.2e-34;  
 Matches 135; Conservative 87; Mismatches 157; Indels 10; Gaps 7;  
 QY 32 TPLQKMEKLSRLDNVILVKREDROPVHSFKRGAYMMAGLTEEOKAHGVITASAGNHA 91  
 DB 23 TPLQKMEKLSRLDNVILVKREDROPVHSFKRGAYMMAGLTEEOKAHGVITASAGNHA 82  
 QY 92 QGVAFSSARLVKALIVMPTATADIKVDVAFRGG--EVLHGANDPEAKAKIELSQ 148  
 DB 83 QGVAFSSARLVKALIVMPTATADIKVDVAFRGG--EVLHGANDPEAKAKIELSQ 142  
 QY 149 QGFTWVPFPHMPTVIAQGGTALAELOQ-DAHMDRVNVPVGGGGLAGAVNLKQMLPQI 207  
 DB 143 HKTFFHFPDQEKVIAQGGTALAELOQ-DAHMDRVNVPVGGGGLAGAVNLKQMLPQI 202  
 QY 208 KVIAVEADSACLAALDAGHPVDLPVGLFAEGVAVKRIQDETFRLCOEYLDIDITVDS 267  
 DB 203 KVIAGEPAGAPAMKESLQGVLEKIDYFVDGAAYKAGELFEICQKLEIVLVPE 262  
 QY 268 DATCAAMKDLFEDVRAVAEBSGALALAGMKKYIALHNIRGERLAHLISGANVNFHGLRV 327  
 DB 263 GKICTITLNLVNGQAIYABPAGAMPIALDPF--KDEIKKQTVVCVSGGNNDIGRQEM 320  
 QY 328 SERELGEQRALLAVITPEKSGFLKFC-QLLG-GNSVTEFNFRPADK-NACIFGVGR 384  
 DB 321 RERLIIEGLOHYITVNPQAGALREFLDVLPNDITREYTKKNNKSGNPGALVGE 380  
 QY 385 LSRGLEERKEILLQMLNDGYSVVDLSDE 413

Db 381 LKCD-EDYHRLMDLNKKGFEYREINKNE 408

## RESULT 14

THD1\_LACLA STANDARD; PRT; 416 AA.  
 ID THD1\_LACLA Q02145; O34132; O9CG81;  
 AC 01-JUL-1993 (Rel. 26, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Threonine dehydratase biosynthetic (EC 4.3.1.19) (threonine  
 deaminase).  
 GN ILVA OR ILI227.  
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.  
 NCBI\_TaxID=1360;  
 RX MEDLINE=93015710; PubMed=1400210;  
 RA Godon J.-J., Chopin M.-C., Ehrlich S.D.,  
 RT "Branched-chain amino acid biosynthesis genes in Lactococcus lactis  
 subsp. lactis.";  
 RL J. Bacteriol. 174:6580-6589(1992).  
 RN (2)  
 RP REVISIONS.  
 RA Delorme C., Goupil-Feuillera N., Godon J.-J., Ehrlich S.D.,  
 RL Renault P.;  
 RN Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IL1403;  
 RX MEDLINE=21235186; PubMed=11337471;  
 RA Bolotin A., Mincker P., Manger S., Jallion O., Malame K.,  
 RT Weisenbach J., Ehrlich S.D., Sorokin A.;  
 RL "The complete genome sequence of the lactic acid bacterium Lactococcus  
 lactis ssp. lactis IL1403.";  
 RN Genome Res. 11:731-753(2001).  
 CC -1- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from  
 threonine in a two-step reaction. The first step is a dehydration  
 of threonine, followed by rehydration and liberation of ammonia.  
 CC -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).  
 CC -1- COFACTOR: Pyridoxal phosphate.  
 CC -1- PATHWAY: Isoleucine biosynthesis; first step.  
 CC -1- SUBUNIT: Homotetramer (by similarity).  
 CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.  
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 or send an email to [license@sb-sib.ch](mailto:license@sb-sib.ch)).  
 CC EMBL: U92974; AAB81922.1; -  
 DR EMBL: AEO06354; AAK05325.1; -  
 DR PIR: C86778; C86778.  
 DR HSSP: P04968; 11DU.  
 DR InterPro: IPR001926; B6\_enzyme\_beta.  
 DR InterPro: IPR000634; S/T\_dehydrase.  
 DR Pfam: PF00291; PALP\_1.  
 DR Pfam: PF00585; Thr\_dehydrat\_C\_1.  
 DR PROSITE: PS00165; DEHYDRATASE\_SER\_THR\_1.  
 KW Isoleucine biosynthesis; lyase; pyridoxal phosphate;  
 KM Complete proteome.  
 FT BINDING 51 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 FT CONFLICT 345 A -> S (IN REF. 1).  
 FT CONFLICT 393 D -> N (IN REF. 1).  
 FT CONFLICT 406 H -> R (IN REF. 1).  
 SQ SEQUENCE 416 AA; 45577 MW; AFDAC61464D7E977 CRC64;

Query Match 22.8%; Score 600; DB 1; Length 416;  
 Best Local Similarity 37.4%; Pred. No. 2,2e-33;  
 Matches 137; Conservative 73; Mismatches 142; Indels 14; Gaps 7;

QY 32 TPLOKMEKTLSSRLDNVILVKREDROPVHSFPLRGAYAMAGTEOKAHGVITASAGNHA 91  
 DB 21 TPLODPLYSNRYQANTYLKEENLQKRSFYLKRGATYISIKLSDEOKSGYVCSAGNHA 80  
 QY 92 QGVAFSSARLGVKALVMPATYADIKYDAVAFGE--VLLHGANFDEAKAKAIELSQ 148  
 DB 81 QGVAFANQVNIISATIEFVPTTPNOKISQVAFEGSHVITILIGTLPDESARAAAFSD 140  
 QY 149 QGFTWVPFDPHPTVYAGGTLALIEL---QGDALHDPVFPVGGGGLAAGVAVILKDM 204  
 DB 141 NDKPFIDPFDEENYVAGGTALIEFPAQAKQGISLDKIFVQIGGGGILAGITAVSKERY 200  
 QY 205 POIKVIAVEADBSACTKALDAGHPVDLPRVGLFAEGVAVKRIGETFRLCOEYLDIT 264  
 DB 201 PQTETIGVEAGATSMKAAVYNSGQPVTLIEHIDKFPADGIAVATVQKTYQLNDKVKOLLA 260  
 QY 265 VDSDAICAMKDLFEDVRAVAPSGALALAGMKXYIALNIRGERLAHILSGANVPHGL 324  
 DB 261 VDEGLISQTLIELVSKLGI VAEPAQATSVALE--LIKDEIKKXIVICIIISGANNDISRM 318  
 QY 325 RYVSERCELGOREALLAVTTIPEEKSGFLK- CQLLG-GRSVTEPNY--RPADAKNACIF 380  
 DB 319 QEIERRAVYVGLKHYFVINFQRPQALRTVSDILGENDITREYIKRADKGGPCL- 377  
 QY 381 VGVRLS 386  
 DB 378 VGILLS 383

## RESULT 15

THD1\_MYCTU STANDARD; PRT; 429 AA.  
 ID THD1\_MYCTU Q10766;  
 AC 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Probable threonine dehydratase biosynthetic (EC 4.3.1.19) (Threonine  
 deaminase).  
 GN ILVA OR RV1559 OR MT1610 OR MYCY48.06C.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 NCBI\_TaxID=1773;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Bignami K., Gas S., Barry C.E. III, Tekaia F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holtroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne W.C., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sulston J.E., Taylor K., Whitehead S., Barrall B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 laboratory strains.";

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
CC - FUNCTION: Catalyzes the formation of alpha-ketobutyrate from  
CC threonine in a two-step reaction. The first step is a dehydration  
CC of threonine, followed by rehydration and liberation of ammonia.  
CC - CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).  
CC - Cofactor: Pyridoxal phosphate (By similarity).  
CC - PATHWAY: Isoleucine biosynthesis; first step.  
CC - SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.  
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CC  
CC -----

DR EMBL; Z74020; CAA98332.1; -  
DR EMBL; AE007027; AAK45877.1; -  
DR PIR; D70763; D70763.  
DR HSSP; P04968; 1TDJ.  
DR TIGR; MT1610; -  
DR TubercuList; Rv1559; -  
DR InterPro; IPR001926; B6\_enzyme\_beta.  
DR InterPro; IPR000634; S/T\_dehydrtse.  
DR InterPro; IPR001721; ThrDh\_C.  
DR Pfam; PF00291; PALP; 1.  
DR Pfam; PF00585; Thr\_dehydrat\_C; 1.  
DR PROSITE; PS00165; DEHYDRATASE\_SER\_THR; 1.  
DR Isoleucine biosynthesis; lyase; Pyridoxal phosphate;  
KW Complete proteome.  
FT BINDING 66 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
FT DOMAIN 145 149 POLY-ALA.  
FT DOMAIN 196 199 POLY-GLY.  
SQ SEQUENCE 429 AA; 45041 MW; DDC761EC258AC521 CRC64;

Query Match 22.0%; Score 578.5; DB 1; Length 429;  
Best Local Similarity 32.3%; Pred. No. 6.4e-32;  
Matches 170; Conservative 71; Mismatches 166; Indels 119; Gaps 15;

QY 4 SQPLSGAP---EGAEYRAVLR-APVEAAQVTPLOKMEKLSRLDNVILVKREDROPV 58  
Db 6 SQSPSSSPLFSLSGADIDRAKRIAPV---VTPTLPSPDRISAITGATVYIKREDIQTV 62  
QY 59 HSFLRGAYAMWAGITFEQKHGVITASAGNHAGVAFSSARLGKALIVMPTATADIKV 118  
Db 63 RSYLRLGAYNLVLQISDELAAGVAVSSAGNHAGFAVACRCIGVHGKRVVPARTPKQKR 122  
QY 119 DAVRGFGE--VLLHGAFDEAKAKAIELSQOQGFVPPDPHPMVIAGGTALAEEL- 174  
Db 123 DRIYHGEFIDLVGSGTVDLAAALAEDEYRTGATVPPFDLRTIAGGTIAVEVLG 182  
QY 175 QQDAHLDRFVVPVGGGILAGVAVLIKQIMPQIKVIAVEADSACLKALDAGHPVDLPR 234  
Db 183 QLEDEPDLVVVPVGGGCIAGITTYLAERTNTAVLGEVPAGAAAMMAALAAAGEPVTLDH 242  
QY 235 VGLFAEGVAVRIQDETFRLCOEYLD--DITVSDAICAMKDLFEDVRAVAPSGALA 292  
Db 243 VDQFVDGAAVRAAGTLLTYAALAAAGDMVSLTVDGAVCTAMLDLYONEGIIABPAGALS 302  
QY 293 LAGMKKYYIALNIRGERLAHILSGANVVFHGLRVYSERCLEGEQREALLAVTIPEKGSF 352  
Db 303 VAGILE-----ADIEPGSTV----- 317  
QY 353 LKFCQLLGRSVTEFNRRFADAKNACIFVGVRLSRGLEERKEILLQMLNDGGYSVVDLSD 412  
Db 318 --VCLISGNN-----DVSRYGEVLERSLVHLGLKHYPLVD----- 351  
QY 413 EMATLHRYVMYWGGRSHPLQERLYSFERPESPGAKLRF--NTLGTWNISLFIH-RSHGT 470  
Db 352 -----FPQEPGALRRFLDDVLDGPNDDITLFEVYKRNRR 384  
QY 471 DYGRVLAFAEXGDHPDPETRLNEL-GYDCHDET---NNPAFRPFL 512

Db 385 ETGEALVGEIIGS-ADLDGILAMRRATDIHVEALEPSPAYRYLL 429

Search completed: December 18, 2003, 15:28:48  
Job time : 18 secs

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OM protein - protein search, using sw model

Run on: December 18, 2003, 15:27:16 ; Search time 21 Seconds

(without alignments)  
2353.843 Million cell updates/sec

Title: NP418220

Sequence: 1 MADSQLSGAPEGAEYLRAV.....LGYDCHDETNNPAPRFLAG 514

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :  
1: pir76:\*  
2: pir1:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2633	100.0	514	1 DMECTS	threonine ammonia-
2	2622	99.6	514	2 B91217	threonine ammonia-
3	2575.5	97.8	515	2 C86063	threonine ammonia-
4	2520	95.7	514	2 AB0924	threonine ammonia-
5	2497	94.8	514	1 DMEBTT	threonine ammonia-
6	2349	85.4	514	2 AG0474	threonine ammonia-
7	1849.5	70.2	510	2 B83374	threonine ammonia-
8	1415.5	53.8	515	2 B83479	threonine ammonia-
9	1410.5	53.6	508	2 B81875	threonine ammonia-
10	1400.5	53.2	508	2 AB1147	threonine ammonia-
11	1380.5	52.4	568	2 E75502	threonine ammonia-
12	1354	51.4	504	2 F83603	threonine ammonia-
13	1318.5	50.1	503	2 A12334	threonine ammonia-
14	1306	49.6	508	1 S77559	threonine ammonia-
15	1212.5	46.1	576	1 DMEBTT	threonine ammonia-
16	1123.5	42.7	600	2 T35116	threonine ammonia-
17	1087	41.3	592	2 T51712	threonine ammonia-
18	994.5	37.8	595	2 A38628	threonine ammonia-
19	937.5	35.6	590	2 T09532	probable threonine
20	646	24.5	422	2 A65644	threonine ammonia-
21	642	24.4	359	2 PQ0468	threonine ammonia-
22	612	23.2	441	2 S35141	probable threonine
23	608	23.1	415	2 G83863	threonine ammonia-
24	600	22.8	416	2 C86778	threonine ammonia-
25	594	22.6	422	2 C89998	threonine ammonia-
26	590.5	22.4	422	2 AG1323	threonine dehydrat
27	580.5	22.0	416	2 F97922	dihydroxy-acid deh
28	580.5	22.0	416	2 B95052	threonine dehydrat
29	578.5	22.0	429	2 D70673	threonine ammonia-

30	577.5	21.9	422	2 AH1694	threonine dehydrat
31	577	21.9	427	2 C87060	threonine deaminas
32	566	21.5	495	2 H84359	threonine dehydrat
33	558.5	21.2	403	2 D81355	threonine ammonia-
34	556	21.1	401	2 D72386	threonine ammonia-
35	551	20.9	419	2 A13368	threonine ammonia-
36	549	20.9	436	2 A47044	threonine ammonia-
37	533	20.2	329	2 AB0897	threonine ammonia-
38	529	20.1	329	1 DMECTD	threonine ammonia-
39	529	20.1	329	2 D85973	threonine ammonia-
40	529	20.1	329	2 E91128	threonine ammonia-
41	521	19.8	424	2 AB2725	threonine dehydrat
42	521	19.8	437	2 F97506	threonine dehydrat
43	516	19.6	405	2 D90166	hypothetical prote
44	512.5	19.5	400	2 AB7700	threonine dehydrat
45	512	19.4	320	2 E83310	L-serine ammonia-1

## ALIGNMENTS

## RESULT 1

DMECTS  
threonine ammonia-lyase (EC 4.3.1.19), biosynthetic - Escherichia coli (strain K-12)  
N:Alternate names: L-serine dehydratase; serine deaminase; threonine deaminase  
C:Species: Escherichia coli  
C>Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #text change 21-Jun-2002  
C:Accession: B27310; C26287; E26570; S48895; S30670; I41304; G65180  
R:COX, J.L.; Cox, B.D.; Fidanza, V.; Calhoun, D.H.  
Gene 56, 185-198, 1987  
A:Title: The complete nucleotide sequence of the *ilvG* gene cluster of Escherichia coli K-12  
A:Reference number: A91578; MUID:88056322; PMID:3315862  
A:Accession: B27310  
A:Molecule type: DNA  
A:Residues: 1-514 <COX>  
A:Cross-references: GB:M32253  
A:Experimental source: Strain K12  
R:Wek, R.C.; Hatfield, G.W.  
J. Biol. Chem. 261, 2441-2450, 1986  
A:Title: Nucleotide sequence and in vivo expression of the *ilvY* and *ilvC* genes in Escherichia coli K-12  
A:Reference number: A92575; MUID:86111952; PMID:3003115  
A:Accession: C26287  
A:Molecule type: DNA  
A:Residues: 439-514 <WEK>  
A:Cross-references: GB:K03503  
A:Experimental source: Strain K12  
R:Lawther, R.P.; Wek, R.C.; Lopes, J.M.; Pereira, R.; Tailon, B.E.; Hatfield, G.W.  
Nucleic Acids Res. 15, 2137-2155, 1987  
A:Title: The complete nucleotide sequence of the *ilvG* gene cluster of Escherichia coli K-12  
A:Reference number: A26570; MUID:87174741; PMID:3550695  
A:Accession: E26570  
A:Molecule type: DNA  
A:Residues: 1-242, 'G', 244-514 <LAW1>  
A:Cross-references: GB:M32253; NID:G146465; PIDN:AAA24024.1; PID:G146470  
R:Lawther, R.P.  
submitted to the EMBL Data Library, December 1987  
A:Reference number: S48893  
A:Accession: S48895  
A:Molecule type: DNA  
A:Residues: 1-514 <LAW2>  
A:Cross-references: EMBL:X04890; NID:G286528; PIDN:CAA28577.1; PID:G286533  
R:Danielis, D.L.; Plunkett III, G.; Burland, V.; Blattner, F.R.  
Science 257, 771-778, 1992  
A:Title: Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 to 85.5  
A:Reference number: S30670; MUID:92358234; PMID:1379743  
A:Accession: S30670  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-121, 'X', 123-139, 'R', 141-514 <DMN>  
A:Cross-references: EMBL:M87049; NID:G836656; PIDN:AAA67575.1; PID:G148179  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1992  
R:Lopes, J.M.; Lawther, R.P.  
Gene 76, 255-269, 1989





A:Molecule type: DNA  
 A:Residues: 1-515 <STO>  
 A:Cross-references: GB:AF005174; NID:g12518630; PIND:RAG58967.1; GSPDB:GN00145; UMGF:Z55  
 A:Experimental source: strain 0157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: ilvA  
 C:Superfamily: threonine dehydratase  
 C:Keywords: ammonia-lyase; carbon-nitrogen lyase

Query Match 97.8%; Score 2575.5; DB 2; Length 515;  
 Best Local Similarity 98.1%; Pred. No. 1.3e-172;  
 Matches 505; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

```

Oy 1 MADQPSLGAPEGAAYLRVAVLRAPVYEAQVTPLOKMKLSSRLDNVILVREDRQPVHS 60
Db 1 MADQPSLGAPEGAAYLRVAVLRAPVYEAQVTPLOKMKLSSRLDNVILVREDRQPVHS 60
Oy 61 FKLNGAYAMMAGLTREQKAGVITASAGNHAQGVAFSSARLGVKALIVPTATADIKVA 120
Db 61 FKLNGAYAMMAGLTREQKAGVITASAGNHAQGVAFSSARLGVKALIVPTATADIKVA 120
Oy 121 VRGGEVLHGAFNDEKAKAIELSQOQGFVWPDPHPVIAAGQTLAELAQDPAHL 180
Db 121 VRGGEVLHGAFNDEKAKAIELSQOQGFVWPDPHPVIAAGQTLAELAQDPAHL 180
Oy 121 VRGGEVLHGAFNDEKAKAIELSQOQGFVWPDPHPVIAAGQTLAELAQDPAHL 180
Db 121 VRGGEVLHGAFNDEKAKAIELSQOQGFVWPDPHPVIAAGQTLAELAQDPAHL 180
Oy 181 DRVFPVGGGLAAGVAVLTKQMPQIKVIAVEADSACLKAALDAGHPVDLPVGLPAE 240
Db 181 DRVFPVGGGLAAGVAVLTKQMPQIKVIAVEADSACLKAALDAGHPVDLPVGLPAE 240
Oy 241 GVAAYKRIQDETFRICQERYLDIITVSDAICAMKDLFEDVRAVAEESGALALAGMKKYI 300
Db 241 GVAAYKRIQDETFRICQERYLDIITVSDAICAMKDLFEDVRAVAEESGALALAGMKKYI 300
Oy 301 ALHNIRGERLAHIIISGANVNFHGLRYVSECELGEOREBALLAVTIPEKSGFLFCOLL 359
Db 301 AOHNIRMTGVAHIIISGANVNFHGLRYVSECELGEOREBALLAVTIPEKSGFLFCOLL 360
Oy 360 GRSVTEFNYPADAKNA CIFGVRLSRGLEERKEIILQMLNDGYSVVDLSDEMAKLVH 419
Db 360 GRSVTEFNYPADAKNA CIFGVRLSRGLEERKEIILQMLNDGYSVVDLSDEMAKLVH 420
Oy 420 RYMGGRPSHPLOEELYSFEPESPQAKLRPLNTLGTWNISLFYRSHGTDYGVLAFAE 479
Db 420 RYMGGRPSHPLOEELYSFEPESPQAKLRPLNTLGTWNISLFYRSHGTDYGVLAFAE 480
Oy 480 EXGDHEPDPETRLNDELGYDCHDETNNPAPRFPLAG 514
Db 480 EXGDHEPDPETRLNDELGYDCHDETNNPAPRFPLAG 515

```

## RESULT 4

AB0924  
 threonine ammonia-lyase (EC 4.3.1.19) [similarity] - *Salmonella enterica* subsp. *enterica*  
 C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 A:Note: this species has also been called *Salmonella typhi*  
 C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 C:Accession: AB0924  
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.  
 Nature 413, 848-852, 2001  
 A:Authors: Park, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhimurium  
 A:Reference number: AF0502; MUID:21534947; PMID:11677608  
 A:Accession: AB0924  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-514 <PAR>  
 A:Cross-references: GB:AL513382; PIND:CAD09412.1; PID:g16504530; GSPDB:GN00176  
 C:Genetics:  
 A:Gene: STY3652  
 C:Superfamily: threonine dehydratase  
 C:Keywords: ammonia-lyase; carbon-nitrogen lyase

Query Match 95.7%; Score 2520; DB 2; Length 514;  
 Best Local Similarity 94.9%; Pred. No. 1e-168;  
 Matches 488; Conservative 18; Mismatches 8; Indels 0; Gaps 0;

```

Oy 1 MADQPSLGAPEGAAYLRVAVLRAPVYEAQVTPLOKMKLSSRLDNVILVREDRQPVHS 60
Db 1 MADQPSLGAPEGAAYLRVAVLRAPVYEAQVTPLOKMKLSSRLDNVILVREDRQPVHS 60
Oy 61 FKLNGAYAMMAGLTREQKAGVITASAGNHAQGVAFSSARLGVKALIVPTATADIKVA 120
Db 61 FKLNGAYAMMAGLTREQKAGVITASAGNHAQGVAFSSARLGVKALIVPTATADIKVA 120
Oy 121 VRGGEVLHGAFNDEKAKAIELSQOQGFVWPDPHPVIAAGQTLAELAQDPAHL 180
Db 121 VRGGEVLHGAFNDEKAKAIELSQOQGFVWPDPHPVIAAGQTLAELAQDPAHL 180
Oy 121 VRGGEVLHGAFNDEKAKAIELSQOQGFVWPDPHPVIAAGQTLAELAQDPAHL 180
Db 121 VRGGEVLHGAFNDEKAKAIELSQOQGFVWPDPHPVIAAGQTLAELAQDPAHL 180
Oy 181 DRVFPVGGGLAAGVAVLTKQMPQIKVIAVEADSACLKAALDAGHPVDLPVGLPAE 240
Db 181 DRVFPVGGGLAAGVAVLTKQMPQIKVIAVEADSACLKAALDAGHPVDLPVGLPAE 240
Oy 241 GVAAYKRIQDETFRICQERYLDIITVSDAICAMKDLFEDVRAVAEESGALALAGMKKYI 300
Db 241 GVAAYKRIQDETFRICQERYLDIITVSDAICAMKDLFEDVRAVAEESGALALAGMKKYI 300
Oy 301 ALHNIRGERLAHIIISGANVNFHGLRYVSECELGEOREBALLAVTIPEKSGFLFCOLL 360
Db 301 AOHNIRMTGVAHIIISGANVNFHGLRYVSECELGEOREBALLAVTIPEKSGFLFCOLL 360
Oy 361 GRSVTEFNYPADAKNA CIFGVRLSRGLEERKEIILQMLNDGYSVVDLSDEMAKLVH 420
Db 361 GRSVTEFNYPADAKNA CIFGVRLSRGLEERKEIILQMLNDGYSVVDLSDEMAKLVH 420
Oy 421 YMGGRPSHPLOEELYSFEPESPQAKLRPLNTLGTWNISLFYRSHGTDYGVLAFAE 480
Db 421 YMGGRPSHPLOEELYSFEPESPQAKLRPLNTLGTWNISLFYRSHGTDYGVLAFAE 480
Oy 481 XGDHEPDPETRLNDELGYDCHDETNNPAPRFPLAG 514
Db 481 LGDHEPDPETRLNDELGYDCHDETNNPAPRFPLAG 514

```

## RESULT 5

DWERT  
 threonine ammonia-lyase (EC 4.3.1.19), biosynthetic - *Salmonella typhimurium*  
 N:Alternate names: L-serine dehydratase; serine deaminase; threonine deaminase  
 C:Species: *Salmonella typhimurium*  
 C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 21-Jun-2002  
 C:Accession: J0278  
 R:Tailon, B.E.; Little, R.; Lawther, R.P.  
 Gene 63, 245-252, 1988  
 A:Title: Analysis of the functional domains of biosynthetic threonine deaminase by complementation  
 A:Reference number: J0278; MUID:88255870; PMID:3230055  
 A:Accession: J0278  
 A:Molecule type: DNA  
 A:Residues: 1-514 <TAI>  
 A:Cross-references: GB:M26670; NID:g341512; PIND:AAA27150.1; PID:g514966  
 A:Note: the authors translated the codon CTG for residue 169 as Ile  
 C:Genetics:  
 A:Gene: ilvA  
 A:Map position: 83 min  
 C:Function: catalyzes the deamination of threonine to yield alpha-ketobutyrate and ammonia  
 A:Description: catalyzes the deamination of threonine to yield alpha-ketobutyrate and ammonia  
 A:Pathway: isoleucine-valine biosynthesis  
 A:Note: this is the first enzyme in the isoleucine biosynthetic pathway  
 C:Superfamily: threonine dehydratase  
 C:Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; isol  
 P:62/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match 94.8%; Score 2497; DB 1; Length 514;  
 Best Local Similarity 94.0%; Pred. No. 4.1e-167;  
 Matches 483; Conservative 18; Mismatches 13; Indels 0; Gaps 0;



253 RLCOEYLDITVDSDAICAMKDLFEDVRAVAPSGALALAGKRYTALHNINGERLAAH 312  
 248 RLCOYIDGHVTVSSDEICAAVKDIFEDTRAIAPSPGALALAGKFAEQOQLGKT 307  
 313 ILSGANNVPHGLRYVSECELGEOREALLANTIPBEKSPFKFOLLGSGSVTEFNTRFA 372  
 308 VLSGANNVPHGLRYVSECELGEOREALLANTIPBEKSPFKFOLLGSGSVTEFNTRFA 367  
 373 DAKNACIVGVRLSGLEERKEILQMLNDGYSVVDLSDDEMAKTLHYRVYVWGGRPSHPLO 432  
 368 DDOLANITVGVRLVGGPDELKSTIHELKQSGYVQVODSDDEMAKTLHYRVYVWGGRPSHPLO 427  
 433 ERLVSFEPPESPGAXLRFPLNTIGTYWNISLPHYRSHGTDYGRVLAAREXGDHEPD--FB 489  
 428 ERLVSFEPPESPGAXLRFPLNTIGTYWNISLPHYRSHGTDYGRVLAAREXGDHEPD--FB 485  
 490 TRINELGYDCHDETNNPAFFFLA 513  
 486 EHLVELGYRYKDETDNPAFFFLA 509

RESULT 8

B63479  
 threonine dehydratase, biosynthetic PA1326 [imported] - Pseudomonas aeruginosa (strain F  
 C:Species: Pseudomonas aeruginosa  
 C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 03-Jun-2002  
 C:Accession: B63479  
 R:Stover, C.K.; Plam, X.O.; Eryin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,  
 .; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
 A:Reference number: A82950; MUID:20437337; PMID:10984043  
 A:Accession: B63479  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-515 <STD>  
 A:Cross-references: GB:AE004562; GB:AE004091; NID:9947263; PIDN:AG04715.1; GSPDB:GN001  
 A:Experimental source: strain PA01  
 C:Genetics:  
 A:Gene: 11VA2; PA1326  
 A:Superfamily: threonine dehydratase

Query Match 53.8%; Score 1415.5; DB 2; Length 515;  
 Best Local Similarity 54.4%; Pred. No. 2.2e-91;  
 Matches 279; Conservative 95; Mismatches 132; Indels 7; Gaps 3;

1 MADSQPSGAEAGAYRAVYEAQVTPLOKMEKLSRLDNLVLRKEDROPVHS 60  
 6 LSAKPLL-----AGYESTLAAPVYDAVETPLQVAPQSLQRLGNVTLKRELDQPVFS 60  
 61 FKLKGAATAMAGLTBEQGAHVITASAGNHAQVAFSSARLGVKALYMPATADIKYDA 120  
 61 FKIGAAITRVARLDEQCARGVITASAGNHAQVAFSSARLGVKALYMPATADIKYDA 120  
 121 VRGSGEVLTHGAMPDEAKATIELSQOQGFVWPDPHPMTVAGGTLALBLQDAH 179  
 121 VLAAGGELLHGDAPPDALAHALQLAEREGMTFVPDPDPAVIAAGQVIAAEITLRHSGR 180  
 180 LDRVFPVGGGLAGAVAVLIKOLMPOIKVIAVAEDSACLKALDGHPRVGLFA 239  
 181 LDAIFVPVGGSLIAGIAAYVKGRLPDIRIVIGVEPEDSNCQALLAAGERVVLQGVIFA 240  
 240 EGVAVKRGDETFRLCOEYLDITVDSDAICAMKDLFEDVRAVAPSGALALAGKRYTALHNINGERL 299  
 241 DGVAVAOIGACNFEVCCKHDEVITVGSDEICAAIKDIDTRISITBPGALAAVAGIKKY 300  
 300 IALHNINGERLAAHILSGANNVPHGLRYVSECELGEOREALLANTIPBEKSPFKFOLL 359  
 301 VABERTEQITVALDSGANINFDRLRHAERABELEGOREALITAVTVAERPSFAFCAAL 360  
 360 GGRSVTEFNTRFAAKNACIVGVRLSGLEERKEILQMLNDGYSVVDLSDDEMAKTLHY 419

Db 361 GRROITEFNRYHSDROAHFLVGVOHPLTDSRADLILAGIEGQFPVLDLTNEMAKLHI 420  
 QY 420 RYVWGGRRPSHPLEERLYSFEPPESPGAXLRFPLNTIGTYWNISLPHYRSHGTDYGRVLAAR 479  
 Db 421 RHWVGHGHTVERREKRFREFPERPGALALFNLKLSRMTISLPHYRNHGAADGRVLAAGL 480  
 QY 480 EXGDHE-PDEFRLNDELGYDCHDETNNPAFFFLA 511  
 Db 481 QVPDEERGELEALQALIGYVWETETNNPAFFFLA 513

RESULT 9

E81875  
 threonine ammonia-lyase (EC 4.3.1.19) NMA1096 [similarity] - Neisseria meningitidis (stre  
 C:Species: Neisseria meningitidis  
 C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 21-Jun-2002  
 C:Accession: E81875  
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
 ; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
 Nature 404, 502-506, 2000  
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
 A:Reference number: A81775; NUID:20222556; PMID:10761919  
 A:Accession: E81875  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-508 <PAR>  
 A:Cross-references: GB:AL162755; GB:AL157959; NID:97379742; PIDN:CA84359.1; PID:97379791  
 A:Experimental source: serogroup A, strain Z2491  
 C:Genetics:  
 A:Gene: 11VA; NMA1096  
 A:Superfamily: threonine dehydratase  
 C:Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; phos  
 P;56/Binding site: pyridoxal phosphate (lye) (covalent) #status predicted

Query Match 53.6%; Score 1410.5; DB 2; Length 508;  
 Best Local Similarity 55.6%; Pred. No. 4.8e-91;  
 Matches 280; Conservative 85; Mismatches 132; Indels 7; Gaps 4;

14 AEYLRATLRAPVYEAQVTPLOKMEKLSRLDNLVLRKEDROPVHSFKLRGAYMMAGL 73  
 8 SNYLIRLTASVVDVAVETPPEPARSLSVLKNLILKRELDQPVFSFKLRGAYMMAGL 67  
 74 TEOKAGVITASAGNHAQVAFSSARLGVKALYMPATADIKYDAVARGGEVLHGA 133  
 68 PKALACGVTAABAGNHAQVAFSSARLGVKALYMPATADIKYDAVARGGEVLHGA 127  
 134 NPDEAKATIELSQOQGFVWPDPHPMTVAGGTLALBLQDAHLD--RVFVPGGG 190  
 128 SYNDAYDVAWELAEQGLTIAFPDDPDVIAAGGTGMEIVSQ--HPDPIRAVFPVIGG 185  
 191 GLAAGVAVLIKOLMPOIKVIAVAEDSACLKALDGHPRVGLFAEGVAVKRGIDE 250  
 186 GLAAGVAVLIKOLMPOIKVIAVAEDSACLKALDGHPRVGLFAEGVAVKRGIDE 245  
 251 TPRLCOEYLDITVDSDAICAMKDLFEDVRAVAPSGALALAGKRYTALHNINGERL 310  
 246 TPRLCOEYLDITVDSDAICAMKDLFEDVRAVAPSGALALAGKRYTALHNINGERL 305  
 311 AHLISGANNVPHGLRYVSECELGEOREALLANTIPBEKSPFKFOLLGSGSVTEFNTR 370  
 306 IAVTSANNVPHGLRYVSECELGEOREALLANTIPBEKSPFKFOLLGSGSVTEFNTR 365  
 371 PADAKNACIVGVRLSGLEERKEILQMLNDGYSVVDLSDDEMAKTLHYRVYVWGGRPSHP 430  
 366 YGDEKRAHIFVGLQ--AAGPDQDLAVISGRIDEALPVDLDDBIATIHIRYVWGGRDXY 424  
 431 LOERLYSFEPPESPGAXLRFPLNTIGTYWNISLPHYRSHGTDYGRVLAAREXGDHE-PDEF 489  
 425 ENERLYSFEPPESPGAXLRFPLNTIGTYWNISLPHYRSHGTDYGRVLAAREXGDHE-PDEF 484  
 490 TRINELGYDCHDETNNPAFFFLA 513  
 485 GFLSLGYSYHEETQNAAYKFLFA 508

RESULT 10  
A81147  
theonine ammonia-lyase (EC 4.3.1.19) NMB0878 [similarity] - *Neisseria meningitidis* (str  
C/Species: *Neisseria meningitidis*  
C/Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 21-Jun-2002  
C/Accession: A81147  
R/Retellin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Hatt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
rt, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masiatani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A/Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.  
A/Reference number: A81000; MUID:2015755; PMID:10710307  
A/Accession: A81147  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-508 <RET>  
A/Cross-references: GB:AE002440; GB:AE002098; NID:97226112; PIDN:AAF41289.1; PID:9722611  
A/Experimental source: serogroup B, strain MC58  
C/Genetics:  
A/Gene: NMB0878  
C/Superfamily: theonine dehydratase  
C/Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; phos  
F/116/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match 53.2%; Score 1400.5; DB 2; Length 508;  
Best Local Similarity 55.0%; Pred. No. 2,4e-90;  
Matches 277; Conservative 89; Mismatches 131; Indels 7; Gaps 4;

14 AEYLRAVLRAPVYEAQAQVTPLOKMKLSRLDNVILVKREDROPVHSGFKRGVYAAWAGI 73  
8 SDPLRLILTRAVDVAVETPPLPARSLSVLKNILKRDLPVPSFKRGVYAAWAGI 67  
74 TEEQKAGVITTSAGNHAQVAFSSARLGVKALIMPTATADIKVDAVVRGEGEVLLHGA 133  
68 KHALACGVIAASAGNHAQVAFSSARLGVKALIMPTATADIKVDAVVRGEGEVLLHGA 127  
134 NFEDEAKAKAELSQQOQFTWPPPHDPVIAAGCTTALBELLODAHLN--RVFVPGG 190  
128 SYNDADVYMELEKEGELTYIAEPDPDVIAGQTVGMEIVSQ--HPDPIRAVFPVIGG 185  
191 GLAAGVAVILKOLMPOIKVIAVEAEDSACLKALDGHPRDLPVGFPAEGVVRKIGDE 250  
186 GLAAGVAVILKOLMPOIKVIAVEAEDSACLKALDGHPRDLPVGFPAEGVVRKIGDE 245  
251 TFRLOEYLDITTVSDAICAAKMDLFEDVRAVAPSGALALAGMKKTYALTANIGERL 310  
246 TFRLOEYLDITTVSDAICAAKMDLFEDVRAVAPSGALALAGMKKTYALTANIGERL 305  
311 AHTLSGANVPHGLRVSRCELGEOREALLAVTIPBEKGSFLKCOLLGGSVTEPNTR 370  
306 IAVTSGANVPHGLRVSRCELGEOREALLAVTIPBEKGSFLKCOLLGGSVTEPNTR 365  
371 FAANAKACITVGRVRLSGLEERKEILLQMDNGSVYVDSDDMAKLVHRYVMGGRPSH 430  
366 YGDEKRAHIFVQ--AAQPODLAVIGSRLEAGIPNVDLTNNELAKIHKHYMGGRITDX 424  
431 LOERLYSFEPPSPGALIRFLNTLGTWNISLFHRSHTDYGRVLAAPKGDHE--PDPE 489  
425 ENERLYSFEPPSPGALIRFLNTLGTWNISLFHRSHTDYGRVLAAPKGDHE--PDPE 484  
490 TRINELGYDCHDETNNPAFRPFLA 513  
485 GFLESIGSYHEETONAAVYKFLA 508

RESULT 11  
E75502  
theonine ammonia-lyase (EC 4.3.1.19) DR0567 [similarity] - *Deinococcus radiodurans* (str  
C/Species: *Deinococcus radiodurans*  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jun-2002

C/Accession: E75502  
R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A/Title: Genome sequence of the radioreistant bacterium *Deinococcus radiodurans* R1.  
A/Reference number: A75250; MUID:20036896; PMID:10567266  
A/Accession: E75502  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-568 <WHI>  
A/Cross-references: GB:AE003915; GB:AE00513; NID:96458262; PIDN:AAF10147.1; PID:9645826  
A/Experimental source: strain R1  
C/Genetics:  
A/Gene: DR0567  
A/Map position: 1  
C/Superfamily: theonine dehydratase  
C/Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; phos  
F/116/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match 52.4%; Score 1380.5; DB 2; Length 568;  
Best Local Similarity 53.8%; Pred. No. 7e-89;  
Matches 276; Conservative 92; Mismatches 134; Indels 11; Gaps 4;

6 PLSGAPEGAELVLRAPVYEAQAQVTPLOKMKLSRLDNVILVKREDROPVHSGFKRG 65  
60 PLPGLDGMDVLRALTSQVGAATETPLSPAPRLSERSGNRVLLKREDQPIFSFKRG 119  
66 AYAMAGLTEQKAGVITTSAGNHAQVAFSSARLGVKALIMPTATADIKVDAVVRGEG 125  
120 AYNKASQLSAERARAGVICASAGNHAQVAFSSARLGVKALIMPTATADIKVDAVVRGEG 179  
126 GEVILHGNFDEAKAKAELSQQOQFTWPPPHDPVIAAGCTTALBELLODAHLN--RVF 184  
180 AEVILHGSFSDAETFPALALQERGLTVHPDPDVIAGQCTTALBELLODAHLN--RVF 239  
185 VEVGGGGLAAGVAVILKOLMPOIKVIAVEAEDSACLKALDGHPRDLPVGFPAEGVAV 244  
240 VEVGGGGLAAGVAVILKOLMPOIKVIAVEAEDSACLKALDGHPRDLPVGFPAEGVAV 239  
245 KRIGDETRFLCOEYLDITTVSDAICAAKMDLFEDVRAVAPSGALALAGMKKTYALTAN 304  
300 KOVGAATPDLTRRYVDDWVRVTDVCAIKVDPDTRAVIEPAGALVAGIKKTYAATHG 359  
305 INGERLAHLSGANVPHGLRVSRCELGEOREALLAVTIPBEKGSFLKCOLLGGSV 364  
360 LHDRTLVALTGANINPRLRVAERTIEGOREALLAVTIPBEKGSFLKCOLLGGSV 419  
365 TEFNRFADAKNACITVGRVRLSGLEERKEILLQMDNGSVYVDSDDMAKLVHRYVMG 424  
420 TEFNRFADAKNACITVGRVRLSGLEERKEILLQMDNGSVYVDSDDMAKLVHRYVMG 478  
425 GRPSPHLOERLYSFEPPSPGALIRFLNTLGTWNISLFHRSHTDYGRVLAAPKGDHE--PD 484  
479 GRPSPHLOERLYSFEPPSPGALIRFLNTLGTWNISLFHRSHTDYGRVLAAPKGDHE--PD 535  
485 EPD-----FETRLNELGYDCHDETNNPAFRPFL 512  
536 PDALTRFGDPLAGIGPAHDVTSNPAVRLFL 567

RESULT 12  
E75603  
theonine dehydratase, biosynthetic PA0331 [imported] - *Pseudomonas aeruginosa* (strain P  
C/Species: *Pseudomonas aeruginosa*  
C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 03-Jun-2002  
C/Accession: E75603  
R/Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lartig, K.; Lam,  
J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho  
A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: F83603  
 A/Status: preliminary  
 A/Molecule-type: DNA  
 A/Residues: 1-504 <STO>  
 A/Cross-references: GB:AE004471, GB:AE004091, NID:99946176, PIDN:AA003720.1, GSPDB:GN001  
 A/Experimental source: strain PA01  
 C/Genetics:  
 A/Gene: 11val; PA0331  
 C/Superfamily: threonine dehydratase

Query Match 51.4%; Score 1354; DB 2; Length 504;  
 Best Local Similarity 52.6%; Fred. No. 4.3e-87;  
 Matches 263; Conservative 95; Mismatches 140; Indels 2; Gaps 2;

15 EYLRAVLRAVYEAQVTPLOKMEKLSRLDNVILVREDRQVPHSFKLRGAYAMMAGLT 74  
 4 QYVKILTSRYDYVAVETPQPARQLSERLGNQVILKREDLPFPFSLKRAIKVAKVADLT 63  
 Db  
 75 EEOKAHGVITASAGNHAQGVAFSSARLGVKALIVMPATADIKVDVARGGCVLLHGAN 134  
 64 EEEKARGVITASAGNHAQGVAFSSARLGVKALIVMPATADIKVDVARGGCVLLHGAN 123  
 Db  
 135 FDEAKAKAIEISQOQGFVWPFPDHPVIAAGGTIALELL-QQDAHLDVFPVGGGGLA 193  
 124 FPEALNAHLKLVDEKGYTFVHPYDDPTIAGQGVAMEILKQPGRLDAIFVPVGGGLV 183  
 Db  
 194 AGVAVLILKOLMPOIKVIAVEAEDSACLKALDAGHPVDLPVGLFAEGVAVKRIGDETFR 253  
 184 AGIAVAVKRLRPEIKITGVEPDESNCLOAAVAGRRVVLGGVGFADVAAVAGIGQHPD 243  
 Db  
 254 LCOEYLDITTVSDAICAMKDLFEDVRAVAPSGALALAGMKKYIALHNIRGERLAIH 313  
 244 ICKDHVEVITVSDDEICAIKIDYDRTSITERGALAVAGIKKYVREGAEQOTLVAI 303  
 Db  
 314 LSGANVPHGRVYSECELBORREALIATVITPEKGSFLKFCOLLGSRVTEFNYPAD 373  
 304 DSGANVPHGRVYSECELBORREALIATVITPEKGSFLKFCOLLGSRVTEFNYPAD 363  
 Db  
 374 AKNACIFGVRLSGLEERKEILQMLNDGYSVVDLSDEMAKLVHVMGGRSHPLQE 433  
 364 GSEAHIFGVQTHPNDREALVAVLREKGPVLDLTNLEAKIHRMVGSHAVKVSDE 423  
 Db  
 434 RLVSFEFSPGAXLRPLNTLGTWNISLFHYRSHGTDYGRVLAFAEXGDHEPD-FETRL 492  
 424 MVFFPEFPERBGALFNFLTKGGRNISMFRHNGADGVAVAGLVQVPEDEBRLIIPOTL 483  
 Db  
 493 NELGYDCHDETNPAPRFLL 512  
 484 EAIGYPWDETANPAYQLFL 503  
 Db

RESULT 13

AI2334  
 threonine ammonia-lyase (EC 4.3.1.19) [similarity] - Nostoc sp. (strain PCC 7120)  
 C/Species: Nostoc sp. PCC 7120  
 A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C/Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
 C/Accession: AI2334  
 R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchida, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
 DNA Res. 8, 205-213, 2001  
 A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
 A/Reference number: AB1807, MUID:21595285, PMID:11759840  
 A/Accession: AI2334  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-503 <KUD>  
 A/Cross-references: GB:BA000019, PIDN:BA075931.1, PID:917133367, GSPDB:GN00179  
 A/Experimental source: strain PCC 7120  
 C/Genetics:  
 A/Gene: at24232  
 C/Superfamily: threonine dehydratase  
 C/Keywords: ammonia-lyase; carbon-nitrogen lyase

Query Match 50.1%; Score 1318.5; DB 2; Length 503;  
 Best Local Similarity 50.2%; Fred. No. 1.3e-84;  
 Matches 251; Conservative 106; Mismatches 140; Indels 3; Gaps 3;

15 EYLRAVLRAVYEAQVTPLOKMEKLSRLDNVILVREDRQVPHSFKLRGAYAMMAGLT 74  
 4 DYVQILTLARVYDYVAQSPLEVAAPNLSARLNKLLKREDMQSVFSFKLRGAYAMMAGLT 63  
 Db  
 75 EEOKAHGVITASAGNHAQGVAFSSARLGVKALIVMPATADIKVDVARGGCVLLHGAN 134  
 64 PDLLAQGVITASAGNHAQGVAFSSARLGVKALIVMPATADIKVDVARGGCVLLHGAN 123  
 Db  
 135 FDEAKAKAIEISQOQGFVWPFPDHPVIAAGGTIALELL-QQDAHLDVFPVGGGGLA 193  
 124 YDDAIAAROLAEKGLTFHPDHPVIAAGGTIAGIIEILRQVQPFHAIFAVAGGGLI 183  
 Db  
 194 AGVAVLILKOLMPOIKVIAVEAEDSACLKALDAGHPVDLPVGLFAEGVAVKRIGDETFR 253  
 184 SGIAVAVKRLRPEIKITGVEPDAANQSLQAGKRVRLSQVGLFADGVAVREVGDETFR 243  
 Db  
 254 LCOEYLDITTVSDAICAMKDLFEDVRAVAPSGALALAGMKKYIALHNIRGERLAIH 313  
 244 LCOEYVDEIILVDTDDCAAIKQVFEEDTSILPEAGALAIAGKAYVEREQIGQOTLVAV 303  
 Db  
 314 LSGANVPHGRVYSECELBORREALIATVITPEKGSFLKFCOLLGSRVTEFNYPAD 373  
 304 ACGANVPHGRVYSECELBORREALIATVITPEKGSFLKFCOLLGSRVTEFNYPAD 363  
 Db  
 374 AKNACIFGVRLSGLEERKEILQMLNDGYSVVDLSDEMAKLVHVMGGRSHPLQE 433  
 364 EKLAHIFIGMQL-QNRADKIHVETFAEGFEILDLTDLTKLHLHMGSHPLAHNE 422  
 Db  
 434 RLVSFEFSPGAXLRPLNTLGTWNISLFHYRSHGTDYGRVLAFAEXGDHE-PDETR 492  
 423 LVRFEFPERBGALMKVASMSPWNISMFRHNGADGVAVAGLVQVPEDEBRLIIPOTL 482  
 Db  
 493 NELGYDCHDETNPAPRFLL 512  
 483 DSGIYQWDESQNPAYQLFL 502  
 Db

RESULT 14

S77559  
 threonine ammonia-lyase (EC 4.3.1.19) - Synechocystis sp. (strain PCC 6803)  
 N/Alternate names: L-threonine deaminase; protein slr2072  
 C/Species: Synechocystis sp.  
 A/Variety: PCC 6803  
 C/Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 21-Jun-2002  
 R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.  
 DNA Res. 3, 109-136, 1996  
 A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis  
 A/Reference number: S74322, MUID:97061201, PMID:8905231  
 A/Accession: S77559  
 A/Status: nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-508 <KBN>  
 A/Cross-references: GB:AB001339, NID:91652360, PIDN:BA17406.1, PID:9165248  
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
 C/Genetics:  
 A/Gene: 11va  
 C/Superfamily: threonine dehydratase  
 C/Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; phos  
 F;51/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted  
 Query Match 49.6%; Score 1306; DB 2; Length 508;  
 Best Local Similarity 50.7%; Fred. No. 9.9e-84;  
 Matches 256; Conservative 96; Mismatches 145; Indels 8; Gaps 4;  
 15 EYLRAVLRAVYEAQVTPLOKMEKLSRLDNVILVREDRQVPHSFKLRGAYAMMAGLT 74







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 18, 2003, 15:27:16 ; Search time 21 Seconds  
(without alignments)  
1035.609 Million cell updates/sec

Title: NP418220  
Perfect score: 2633  
Sequence: 1 MADSQLSGAPGGAFLRAV.....LGYDCHDETNPAPRFLAG 514

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/aa/5A.COMB.pep: \*  
2: /cgn2\_6/ptodata/1/aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/1/aa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/1/aa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/1/aa/PTUS.COMB.pep: \*  
6: /cgn2\_6/ptodata/1/aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1419	53.9	677	4	US-09-252-991A-22442
2	1345	51.1	524	4	US-09-252-991A-27763
3	1277.5	48.5	520	4	US-09-328-352-7451
4	612	23.2	441	1	US-08-403-866-10
5	583.5	22.2	424	1	US-09-134-001C-3876
6	556	21.1	436	3	US-08-669-378-4
7	551	20.9	436	3	US-08-669-378-2
8	550	20.9	411	4	US-09-328-352-5207
9	549	20.9	436	3	US-08-669-378-10
10	549	20.9	436	3	US-08-669-378-12
11	546	20.7	436	3	US-08-669-378-8
12	541	20.5	436	3	US-08-669-378-6
13	512	19.4	374	4	US-09-252-991A-11294
14	449.5	17.1	328	4	US-09-328-352-4536
15	357	13.6	340	4	US-09-789-3300A-2
16	355	13.5	331	4	US-09-252-991A-29333
17	337.5	12.8	329	4	US-09-843-297-2
18	326.5	12.4	325	3	US-09-088-435-1
19	275.5	10.5	378	4	US-09-789-3300A-4
20	211	8.0	367	4	US-09-134-001C-4168
21	205.5	7.8	319	4	US-09-134-001C-3330
22	204.5	7.3	312	4	US-09-134-001C-3920
23	191.5	7.3	461	4	US-09-328-352-5878
24	173.5	6.6	309	4	US-09-724-623-72
25	165	6.3	308	4	US-09-107-532A-3925
26	163	6.2	551	1	US-08-120-960-2
27	163	6.2	551	4	US-09-347-878-9

28	161.5	6.1	403	4	US-09-328-352-5461	Sequence 5461, Ap
29	159	6.0	307	4	US-09-328-352-8179	Sequence 8179, A
30	152	5.8	311	4	US-09-252-991A-25027	Sequence 25027, A
31	150	5.7	748	4	US-09-252-991A-31491	Sequence 31491, A
32	148.5	5.6	382	4	US-09-252-991A-29566	Sequence 29566, A
33	147	5.6	378	4	US-08-311-731A-161	Sequence 161, App
34	143.5	5.5	308	4	US-09-107-532A-6629	Sequence 6629, Ap
35	142	5.4	478	4	US-09-252-991A-16935	Sequence 16935, A
36	140	5.3	335	4	US-09-328-352-5450	Sequence 5450, Ap
37	124.5	4.7	424	4	US-08-311-731A-220	Sequence 220, App
38	121.5	4.6	397	1	US-07-956-697B-5	Sequence 5, Appli
39	121.5	4.6	397	1	US-08-263-098-5	Sequence 5, Appli
40	120.5	4.6	423	4	US-09-328-352-5224	Sequence 5224, Ap
41	119.5	4.5	389	4	US-09-594-193-8	Sequence 8, Appli
42	116	4.4	937	4	US-09-252-991A-32336	Sequence 32336, A
43	115	4.4	612	4	US-09-252-991A-17844	Sequence 17844, A
44	112.5	4.3	443	4	US-09-594-193-9	Sequence 9, Appli
45	110.5	4.2	313	4	US-09-252-991A-28686	Sequence 28686, A

## ALIGNMENTS

RESULT 1  
US-09-252-991A-22442  
; Sequence 22442, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 22442  
; LENGTH: 677  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
; US-09-252-991A-22442

Query Match 53.9%; Score 1419; DB 4; Length 677;  
Best Local Similarity 54.4%; Pred. No. 3.5e-132;  
Matches 280; Conservative 94; Mismatches 133; Indels 8; Gaps 3;

5 OPLSGA-----PGAEYLRARVLRAPYEAQVTPLOKMEKLSRLDVIIVKREDROPV 58  
161 QPMSSTISASKPPLAGVSEILAPVYDAVETPLOWAPOLSOBLKRNVLKREDLOPV 220  
59 HSPFLRGAYVAMAGLTEROKAGVITASAGNHAQGVAFSSARLGKALIVPTATADIKV 118  
221 FSPFKRGVTVARLSDQKRGVITTSAGNHAQGLAAARLGRVAVIVPRTPELKV 280  
119 DAVRFGGEVILHGANPDEAKAKAIEISQCGFTWVPFDPHMYTAGGTLALELQ-D 177  
281 KGVLRGGEALHGAFFDALAHALQLAERGMFVPPYDPDVYAGGTAMETLROHS 340  
178 AHLDRVPVPGGGGLAGVAVLIRKQMPQIVIAVEADSACTKALAGHPVDLPRGL 237  
341 GRLDITFPVPGGSLIAGIAYVYKRLDPIVIGVEPDSNCIOALAAGERVILGQGL 400  
238 FAEQVAVRRIGDETFRLCOEYLDIITVSDPAICAMKDLFEDYRAVAEPGATLAAMK 297  
401 FADGVAQAQICACNPEVCXKHVDEVTIGSDCECAIKDIYDDRSITPEPAGALAVAGC 460  
298 KYIALHNIRGRLAIIISGANVNHGLRYVEERCELGQRALAVTIPPEKGSFLKQCQ 357  
461 KYVARERTGOTLVADISGANINFDRLPHVAERALEGRERAIITAVVAERPGSFKACA 520

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Oy 358 LLGGSSVTEENNRPADAKKACIFVGRVLRSGLEERKEIIQMLNDGVSVDLSDDEAKL 417
Db 521 ALGRQITEENFRYHSDRQAHLFVVGQTPRLTDSRADLLAGLEQGFPLVLDLTNDEAKL 580
Oy 418 HVRVWVGRRSPHLPORLYSFEEPESSGAXLREPLNTLGTWYNI SLPHYNSHGTDYGRVLA 477
Db 551 HIRHVVGGGTIVRRRLRFEPEPEERGALLNLDTKYSRWNISLPHYRNHGAADGRVLA 640
Oy 478 AFEXGDHE-PDPETRLNELGYDCHDERTNPAAPFF 511
Db 641 GLQVPDEERGELEALQATIGRPWETTHNPAKRLF 675

```

RESULT 2  
US-09-252-991A-27783  
, Sequence 27783, Application US/09252991A

1 APPLICANT: Marc J. Rubenfield et al.  
 2 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 3 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 4 FILE REFERENCE: 10/196,136  
 5 CURRENT APPLICATION NUMBER: US/09/252,991A  
 6 PRIOR APPLICATION NUMBER: 1999-02-18  
 7 PRIOR APPLICATION NUMBER: US 60/074,788  
 8 PRIOR FILING DATE: 1998-02-18  
 9 PRIOR APPLICATION NUMBER: US 60/094,190  
 10 PRIOR FILING DATE: 1998-07-27  
 11 NUMBER OF SEQ ID NOS: 33142  
 12 SEQ ID NO 27783  
 13 LENGTH: 524  
 14 TYPE: PRN  
 15 ORGANISM: Pseudomonas aeruginosa  
 16 FEATURE:  
 17 NAME/KEY: UNSURE  
 18 LOCATION: (108)  
 19 OTHER INFORMATION: Identity of amino acid at the above locations are unknown.  
 20 US-09-252-991A-27783

Query Match	Score	DB	Length
51.1%	1345	4	524

Best Local Similarity 52.6%; Pred. No. 5.3e-125;  
Matches 263; Conservative 95; Mismatches 140; Indels 2; Gaps 2

QY 15 EYLRATRAPVYEAQVTPLOKMEKSSRLDNVILVKREDQPVHSFKLKGAYAMAGLT 74

24 QYVKILSRVDAVETPLQPARQISRLGNQVLLKREDLQVFSFKIRGANVKAQLT 83

Qy 75 EÖKAHVITASAGNHOQVAFSSARLVKALIMPTATADIKVDVGFGEVLLHGAN 134

Db 84 EEEKARGVIAASAGNHAQGLALAAKXRGQIRAVIIMPTTPEIKVQAVRAHGAKAVLHGDA 143

```

QY      135 FDEAKAKAIELSQGGGFTWPPFDHPMVIAQGTLLLELL-QDDAHLDHVFVPRVGGGGLA 193
      | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
      | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :

```

DB 144 FPEALAHAKLTVDEKGYTFVHPYDDPTIAGSGVANEILRQPGRLDAIFVPGGGGGLV 203

[illegible]

254 ICOEYI.DDIITVSDAICAMKDI.FEDYRAVAPSGAI.AI.AGKKYI.AI.HNIRGERIAHI 313

```
Db      264 ICKDHVEVITSTDEICAIKIDYDDTSTRTEPAGALAVAGIKKYVEREREAEQOTLVAI 323
```

QY 314 LSGANVFHGLRYVSERCELGQREALLAVTIPEEKGSFLKFCQLLGGSVTEFNRYRAD 373

324 DSGANVAFDRLRHVAERAEGERREALIAVTIPEPSPFKAFCEAVGRQITEFNRYRHS 383

374 AKNACIFVGVRLRGLEERKEILQMINDGYSVVDLSDEMAKIHVRVWVGGRPSHPLOE 433

Db 324 GSEAHIFGVQTHPENDEPREALVALIREKGFVLDLIDNELAKLIRHNVGGHAKVSD 443

434 RLVSFEEPSGAXLRFLNTLTGYWNISLPHYRSHGTDYGRVLAAFEXGDHEPD-FETRL 492

Db 444 MYRFEFFRRPALNPNFLTKLGGRNINSMFYRHNGAAGRGVAGLVPRDEKHLIQTL 503

QY 493 NELGYDCHDETNNPARRFTL 512

Db 504 EAIGYRYMDETANPAYQLFL 523

RESULT 3  
US-09-328-352-7451  
; Sequence 7451, Application US/09328352

```

:
: APPLICANT: Gary L. Breton et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
: TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: GPC99-03PA
: CURRENT APPLICATION NUMBER: US/09/328,352
: CURRENT FILING DATE: 1999-06-04
: NUMBER OF SEQ ID NOS: 8252
: SEQ ID NO 7451
: LENGTH: 520
: TYPE: prt
: ORGANISM: Acinetobacter baumannii
: US-09-328-352-7451

```

Query Match 48.5%; Score 1277.5; DB 4; Length 520;

Base local similarity 31.75; Freq. no. 2,076,110;  
Matches 264; Conservative 86; Mismatches 144; Indels 15; Gaps 5.

17 LRAVLRAPVYEAQVTPDQKMEKLSRRDNLVVKREDRQPVHSFKLRGAYAMAGLTEE 76

Db 13 VRQILQATVYDVAIETPLEAPRISQKLNNTIRKREDLQVFSEFKRGAVNRISQLPE 72

```
0Y      | | | | | | | | | : | : | : | | | | : | |
77 QAHGVITASAGNHQGVAFSSARLGVKALIIMPEATADIKYDAVRGEGEVLHGNFDF 136
```

DB /3 QLEKGVICASAGNHAQVALSGKUGLIPALI VMPSTIPJIKVQAVAKKGGVLEHGSFD 132

133 TANKAACCPAAEEGIVETIPYDDELVIAGGGTINNETIPQWRDVEYEVAVAGGGGIGAGV 192

197 AVLLKQIMPOIKVIAVEABDSACLKALDAGHPVDLPRVGIFAEGVAVKRIGDETFRLCQ 256

Db 193 AAYLGDAVAPHYKVIQVEYEESACLKALEANERVVLPHYGLFADGTAVAQICGLPFEDIVR 252

257 BYLD-----DIITVDSDAICAMKOLFEDYRAVAPSGALALAGMKYIALHNRG 307

Db 253 LRKSPNGPIVEPDIVTNTDEICAAIKDTFDENKRSIVEPSGAMALAGIKKYVAEHKISG 312

308 ERLAHTSGANVNPHGIRYVSEBCELGEORALLAVTIPEKGSFLKCOLLGRSVTEF 367

Db 313 KMWISVCGANNFDRRLRYIAETELGEGREAIYAVTLSEKGAFLGFCRLQGRNITLF 372

QY 368 NYRPADAKNACTFVGVRLSRGEEKELLQMLNDGGYSVVDLSDDMAKTHVRVYMGGRP 427

Db 373 NYRANTBEAQVFVGISLKGKGTERRHEITBQLKQNYVVDLSDDEVAKLHIRYLLIGSHA 432

428 SHPLERLYTEFPESPGAXLRPLNTLGYWNISLFIHYRSHGTGYRVLAAFXEND--HE 485

433 NLD-BERLEFRIEFPEREGALLITFTKLGTHNITLPHKXHGAEKSVLVGQDAIDAKXN 491

486 PU--PBIKINELSIDCHDELINNEPAFRPL 512

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RESULT 4  
US-08-403-866-10

; Sequence 10, Application US/08403866  
; Patent No. 5643779

```

; GENERAL INFORMATION:
;
; APPLICANT: Enrich, Stanislav

```

APPLICANT: Godon, Jean-Vacques

APPLICANT: Renault, Pierre  
TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate  
TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate  
NUMBER OF SEQUENCES: 16  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,866  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 20747/30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1600  
TELEFAX: (716) 263-1487  
TELEX: 978450 (WUT)  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Lactococcus lactis subsp. lactis  
INDIVIDUAL ISOLATE: ILVA  
US-08-403-866-10

Query Match 23.2%; Score 612; DB 1; Length 441;  
Best Local Similarity 37.2%; Pred. No. 3.2e-52;  
Matches 143; Conservative 74; Mismatches 151; Indels 16; Gaps 8;  
QY 16 YLRVLRAPVY--EAAQVTPLOKMEKLSRLDNVILVREDRQPVHSFKLRGAYAMAGL 73  
DB 28 YLSNRYQNTYLRKEVYTKTPLOLDPLYSNKYQANTYLRKEVILKVRSLKRGAYYSISKL 87  
QY 74 TEOKAHGVTASAGNHAGVAFSSARLGVKALIVPTATADIKVDVAFGG--EVLHG 130  
DB 88 SDEGRSKVVCASAGNHAGVAFANQINISATIPPTNPQKISQVKEFGESVITRL 147  
QY 131 HGANDEAKAKAIELSQOGFTWVPFDPHMYIAGGTLAELT---QDAHLDVAVP 186  
DB 148 IGDTFDESARAKAFSQNDKRFIDPFDENVIAQGTVALEIFAQAKKGISLDKIFVQ 207  
QY 187 VGGGAGVAVLTKQMPQIKVIAVEADSACTKAALDAGHPVLDPRVGLFAEGVAVKR 246  
DB 208 IGGGGLNGITAYSKERYPTETIIGVEAKGATSMKAAVSACQVLTLEHIDKFDGIAVAT 267  
QY 247 IGDTEFLRCEYLDITVDSDAICAMKDLFEDVRAVAEFGALALAGMKKYIALHNIR 306  
DB 268 VQKTYQVINDKQVLADEGLISQTLIELSKYIAERFAGASVALR--LIKDEIK 325  
QY 307 GERLAHILSGANVNFHGLRYVSERCLEGBREALLAVTIPERKGSFLKFC--QLLGR-GRSV 364  
DB 326 GKNIVCIISGNNDISRMQIEERLALVYEGLKHVFINPQPGSLRFTVSDILGPNDDI 385  
QY 365 TEENY--RFADAKNACIFVGVL 386  
DB 386 TRFEYIKRADKKGKPCPL--VGILLS 408

RESULT 5  
US-09-134-001C-3876  
Sequence 3876, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 3876  
LENGTH: 424  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3876

Query Match 22.2%; Score 583.5; DB 4; Length 424;  
Best Local Similarity 34.8%; Pred. No. 2e-49;  
Matches 137; Conservative 89; Mismatches 145; Indels 23; Gaps 10;  
QY 16 YLRVLRAPVYEAQVTPLOKMEKLSRLDNVILVREDRQPVHSFKLRGAYAMAGL 75  
DB 18 YLR--LKNIVK---TPLOPDHLSQKYNQNVILKEDLOWVRSFKLRGAYMAISVLSN 71  
QY 76 EOKAHGVTASAGNHAGVAFSSARLGVKALIVPTATADIKVDVAFGG--EVLHG 132  
DB 72 EKKKGITCASAGNHAGVAFATKKNLKVAFIPVPTPQKINQVKEFGDSNVEIVLIG 131  
QY 133 ANFEAKAKAIELSQOGFTWVPFDPHMYIAGGTLAELTQ---DAHLDVAVPVG 188  
DB 132 DTFPHCLAQNLNRYKQKRMNFIDPFNNVYTIAGGTLAKELINQAEKEDKTFDVFFAIG 191  
QY 189 VGGGAGVAVLTKQMPQIKVIAVEADSACTKAALDAGHP--VDLPRVGLFAEGVAVKR 247  
DB 192 GGGILSGVSTFKKHSPTKILIGVEPTGASMYGSVINHSIVLENIDKVDGASVAVR 251  
QY 248 GDETFRLCEYLDITVDSDAICAMKDLFEDVRAVAEFGALALAGMKKYIALHNIRG 307  
DB 252 GDITFDLAKQVDVYQVDEGAVGCSITLDVYSKQAIYAEFGALSVSLRGY--KKQIEN 309  
QY 308 ERLAHILSGANVNFHGLRYVSERCLEGBREALLAVTIPERKGSFLKFC--QLLGR-SVT 365  
DB 310 KTVICVISGNNDISRMKIEERSLLEEMHGFYFLNFPQPGALREFVDVLDGPODIT 369  
QY 366 EENYRFADAKN-ACIFGVRLRSLERKEILQM 398  
DB 370 KFEYIKTSQNTGTVIGIQ---LKHDDLIQL 399

RESULT 6  
US-08-669-378-4  
Sequence 4, Application US/08669378  
Patent No. 6107063  
GENERAL INFORMATION:  
APPLICANT: Moeckel, Bettina  
APPLICANT: Eggeling, Lothar  
APPLICANT: Sahm, Hermann  
TITLE OF INVENTION: PRODUCTION OF L-ISOLEUCINE BY MEANS OF  
TITLE OF INVENTION: RECOMBINANT MICROORGANISMS WITH DEREGULATED THREONINE  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/669,378
FILING DATE: 20-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE95/00017
FILING DATE: 09-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 00 926.7
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 016881/0142
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-669-378-4

Query Match      21.1%; Score 556; DB 3; Length 436;
Best Local Similarity 35.8%; Pred. No. 1.2e-46;
Matches 145; Conservative 73; Mismatches 159; Indels 28; Gaps 12;

13 GAEYLRA---VLRAPVEAAQVTPLOKMEKLSRLDNLVLRERDOPVHFKRGAYA 68
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
17 GAELIRAAIDIQTAQRISIVIAFTPLQYCPRISEETGAEIYLRKEDLDVRSYKIRGALN 76
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
69 MNAGLTEBOKAGVITASAGNHAQVAFSSARLGKALIVMPATADIKYDAVRGSGE- 127
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
77 SGAQSPQEBRDAGIVAAAGNHAQVAYCKSLGVGRITVVPQTPKQKRDIMVHGSEF 136
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
128 --VLHGANFDEAKAKAIELSQOQGFVWPDPDHPVIVAGGTLAELLQODANL---D 181
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
137 VSLVTVGNNFDEASAAHEDARTGATLIEPDAKRTVIGGGTVAAEILISQLTSMGKSD 196
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
182 RVFVPPVGGGGLAGVAVLIKQIMPOIKVIAVEABDSACIKALADAGHPVDLPVGLFABG 241
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
197 HVMWPVGGGGLAGVAVSYADNAPRTAIVIGIEPAGAAHQALHNGGPTLLETVDPFVVG 256
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
242 VAVKRIGETFRLCOEYLLDI--ITVDSDAICAMKDLFEDVRAVAPSGALALAGMKKY 299
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
257 AEVKRVDGLNTYITVEKNGRVMHMSATGAVCTEMLDLYONEGIIAEPAGALSIAGLKE- 315
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
300 IALHNIRGERLAHILSGANVNFHGLRY--VSEKCEIGEORALAVTIPBEKGSFLKFCQ 357
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
316 --MSFAPGSAVVCIISGGNNV--LRYAEIAERSLVHRLGKHYFLVNPQKPGQLNHFLE 371
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
358 -LLG-GRSVTEFNY-RFADAKNACIFVGRLSR--GLE--ERKE 394
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372 DILGPDDDITLTFEYLKRNRETGTALVGTHLSAAGLSLDERME 416
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CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,378
FILING DATE: 20-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE95/00017
FILING DATE: 09-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 00 926.7
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 016881/0142
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-669-378-2

Query Match      20.9%; Score 551; DB 3; Length 436;
Best Local Similarity 35.6%; Pred. No. 3.7e-46;
Matches 144; Conservative 73; Mismatches 160; Indels 28; Gaps 12;

13 GAEYLRA---VLRAPVEAAQVTPLOKMEKLSRLDNLVLRERDOPVHFKRGAYA 68
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17 GAELIRAAIDIQTAQRISIVIAFTPLQYCPRISEETGAEIYLRKEDLDVRSYKIRGALN 76
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
69 MNAGLTEBOKAGVITASAGNHAQVAFSSARLGKALIVMPATADIKYDAVRGSGE- 127
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
77 SGAQSPQEBRDAGIVAAAGNHAQVAYCKSLGVGRITVVPQTPKQKRDIMVHGSEF 136
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
128 --VLHGANFDEAKAKAIELSQOQGFVWPDPDHPVIVAGGTLAELLQODANL---D 181
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
137 VSLVTVGNNFDEASAAHEDARTGATLIEPDAKRTVIGGGTVAAEILISQLTSMGKSD 196
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
182 RVFVPPVGGGGLAGVAVLIKQIMPOIKVIAVEABDSACIKALADAGHPVDLPVGLFABG 241
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
197 HVMWPVGGGGLAGVAVSYADNAPRTAIVIGIEPAGAAHQALHNGGPTLLETVDPFVVG 256
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
242 VAVKRIGETFRLCOEYLLDI--ITVDSDAICAMKDLFEDVRAVAPSGALALAGMKKY 299
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
257 AEVKRVDGLNTYITVEKNGRVMHMSATGAVCTEMLDLYONEGIIAEPAGALSIAGLKE- 315
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
300 IALHNIRGERLAHILSGANVNFHGLRY--VSEKCEIGEORALAVTIPBEKGSFLKFCQ 357
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
316 --MSFAPGSAVVCIISGGNNV--LRYAEIAERSLVHRLGKHYFLVNPQKPGQLNHFLE 371
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
358 -LLG-GRSVTEFNY-RFADAKNACIFVGRLSR--GLE--ERKE 394
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
372 DILGPDDDITLTFEYLKRNRETGTALVGTHLSAAGLSLDERME 416
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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APPLICANT: Gary L. Breton et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
 FILE REFERENCE: GTC99-03PA  
 CURRENT APPLICATION NUMBER: US/09/328,352  
 CURRENT FILING DATE: 1999-06-04  
 NUMBER OF SEQ ID NOS: 8252  
 SEQ ID NO 5207  
 LENGTH: 411  
 TYPE: PR  
 ORGANISM: Acinetobacter baumannii  
 US-09-328-352-5207

Query Match 20.9%; Score 550; DB 4; Length 411;  
 Best Local Similarity 35.2%; Pred. No. 4,2e-46;  
 Matches 134; Conservative 79; Mismatches 158; Indels 10; Gaps 6;

QY 32 TPLQKMEKLSRLDNVILVKREDROPVHSPFLRGAYMMAGITBOKAHGYITASAGNHA 91  
 DB 30 TPFVSEETISKTLGKMWLKFENIQFTASFKERGLNLTLSSEKQHGVIASAGNHA 89  
 QY 92 QGVAFSSARLGVKALIVPTATADIKVDVARGFGEVLLHGANFDEAKAKAIEISQOQGF 151  
 DB 90 QGVAYHAGRTGVATITVMPKSTPNVYQVRVEYGARVILHSGDSEAAEMHRYVAQESL 149  
 QY 152 TWVPPEDHPVVIAGGTLALTELQODAHLDVFPVPGGGIAGAVAVLIKOLMPOIKYA 211  
 DB 150 TIIFPDAAELIAGGTLALENLEVPDILVPIIGGGIISGAIATAKINPFIKTIIG 209  
 QY 212 VEADSACLKALADAGHPVDLPRVGLPAEGVAVKRIQDETFRLCOEYLDIITVDSDAIC 271  
 DB 210 VQSVVYPSM-AKLCNVGLAVSMGSTVAEGIAVTPGLTQIAKHFPVDILVVTEDMIE 268  
 QY 272 AAMQDLPEDVAVAPSPGALLAGKKTIALHNIRGERLAHILSGANVFHGLRYVSERC 331  
 DB 269 EAILLNIEKTVCEGAGATGIAAIMSRPD--FLGHKVGAVLISGNDITFVWVSVLQRH 326  
 QY 332 ELGBOREALAVTIPBEKGSFLKFCQLG--GRSVTEFNY-RPA--DAKNACIFVGRL 385  
 DB 327 LTRGRMWRIVELPDNFGALARLTALTAEGCGNIYELRHRAFTSPAKSAVSDIEL 386  
 QY 386 SRGLEERKEILQMLNDGYSV 406  
 DB 387 -KSAPDLEPLIQAMQLEGYIV 406

RESULT 9  
 US-08-669-378-10  
 Sequence 10, Application US/08669378  
 Patent No. 6107063  
 GENERAL INFORMATION:  
 APPLICANT: Moeckel, Bettina  
 APPLICANT: Eggeling, Lothar  
 APPLICANT: Sahm, Hermann  
 TITLE OF INVENTION: PRODUCTION OF L-ISOLEUCINE BY MEANS OF  
 TITLE OF INVENTION: RECOMBINANT MICROORGANISMS WITH DEREGULATED THREONINE  
 TITLE OF INVENTION: DEHYDRATASE  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/669,378  
 FILING DATE: 20-MAR-1997

CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/DE95/00017  
 FILING DATE: 09-JAN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE P 44 00 926.7  
 FILING DATE: 14-JAN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bent, Stephen A.  
 REGISTRATION NUMBER: 29,768  
 REFERENCE/DOCKET NUMBER: 016881/0142  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 672-5300  
 TELEFAX: (202) 672-5399  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 436 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-669-378-10

Query Match 20.9%; Score 549; DB 3; Length 436;  
 Best Local Similarity 35.6%; Pred. No. 5,8e-46;  
 Matches 144; Conservative 73; Mismatches 160; Indels 28; Gaps 12;

QY 13 GAETLRA---VLAPYEAQVTPLOKMEKLSRLDNVILVKREDROPVHSPFLRGAYA 68  
 DB 17 GAELIRADIOTAOARISSVIAFPPLQYCPRLSEETGAETILKREDIDQDVASYKIRGLN 76  
 QY 69 MMAGLTBOKAHGYITASAGNHAQVAFSSARLGVKALIVPTATADIKVDVARGFGE- 127  
 DB 77 SGAQSPQGRDAGVAAASAGNHAGVAVYCKSLGQGRIVPVOTPKOKRDRIMWGGEEF 136  
 QY 128 --VLLHGANFDEAKAKAIEISQOQGFVWPPEDHPVVIAGGTLALTELQODAHL---D 181  
 DB 137 VSLVVTGNPNDEAASAAHEDERTGATLIEPFDARNVIGQGTAAELISQLTSMGSKAD 196  
 QY 182 RVFPVPGGGIAGAVAVLIKOLMPOIKYIAVEADSACLKALADAGHPVDLPRVGLPAEG 241  
 DB 197 HWVPVPGGGIAGAVVYMAQDAPRTAIVGIEPAGASMQAALHNGGFTLETVDLPFYDG 256  
 QY 242 VAVKRIQDETFRLCOEYLDI--ITVDSDAICAMQDLPEDVAVAPSPGALLAGKKTIAL 299  
 DB 257 AEVRVADLNTYIVKQGRVHMMSATGAVCTEMDLVQEGITAEPAQALSTAGLKE- 315  
 QY 300 IALHNIRGERLAHILSGANVFHGLRY--VSERCLEGBOREALAVTIPBEKGSFLKFCQ 357  
 DB 316 --MSFAGSVVVCIIISGNDV--LRYAEIAERSLVHRGLKHYFLVNFPOKRGQLRHLE 371  
 QY 358 -LIG-GRSVTEFNY-RPADAKNACIFVGRLSR--GLE--ERKE 394  
 DB 372 DILPDDITLTFEYLKENNETGTALVGHILSEASGLDSLRLERME 416

RESULT 10  
 US-08-669-378-12  
 Sequence 12, Application US/08669378  
 Patent No. 6107063  
 GENERAL INFORMATION:  
 APPLICANT: Moeckel, Bettina  
 APPLICANT: Eggeling, Lothar  
 APPLICANT: Sahm, Hermann  
 TITLE OF INVENTION: PRODUCTION OF L-ISOLEUCINE BY MEANS OF  
 TITLE OF INVENTION: RECOMBINANT MICROORGANISMS WITH DEREGULATED THREONINE  
 TITLE OF INVENTION: DEHYDRATASE  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington  
 STATE: D.C.

COUNTRY: USA  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/669,378  
 FILING DATE: 20-MAR-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/DE95/00017  
 FILING DATE: 09-JAN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE P 44 00 926.7  
 FILING DATE: 14-JAN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bent, Stephen A.  
 REGISTRATION NUMBER: 29,768  
 REFERENCE/DOCKET NUMBER: 016881/0142  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (1202) 672-5300  
 TELEFAX: (1202) 672-5399  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 436 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

Db 372 DILGDDDTLCEYLKNNRETGTALVGIHLSASGLDILLERNE 416

RESULT 12

US-08-669-378-6

Sequence 6, Application US/08669378

Patent No. 6107063

GENERAL INFORMATION:

APPLICANT: Moeckel, Bettina

APPLICANT: Eggeling, Lothar

APPLICANT: Sahm, Hermann

TITLE OF INVENTION: PRODUCTION OF L-ISOLEUCINE BY MEANS OF

TITLE OF INVENTION: RECOMBINANT MICROORGANISMS WITH DEREGULATED THREONINE

NUMBER OF INVENTIONS: DEHYDRATASE

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/669,378

FILING DATE: 20-MAR-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/DE95/00017

FILING DATE: 09-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 00 926.7

FILING DATE: 14-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 016881/0142

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5339

TELEX: 904136

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 436 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-669-378-6

Query Match 20.5%; Score 541; DB 3; Length 436;

Best Local Similarity 35.3%; Pred. No. 3.6e-45;

Matches 143; Conservative 73; Mismatches 161; Indels 28; Gaps 12;

Db 13 GAEYLR-----VLRAPYEAQVTPLOKMEKLSRLDNVILVKEDRPPVHSGFLRGAYA 68

Db 17 GAEIRADIGTQARISVIAFPPLQYCPRLSEETGAELIYLRKEDIQDVRSYKIRALN 76

Db 69 MMALGTEOKAHGIVITASAGNHAQVAFSSARLGKALIVPTATADIKYDAVAGFGE- 127

Db 77 SGAOSPEQORDAGIVAASAGNHAQVAVCKSLGVQGRIVYVPTPKOKDRIVHGGEE 136

Db 128 --VLLHGANFDEAKAKAIELSQOQFTWVPFDPHVMVIAQGTALALELQDAHL---D 181

Db 137 VSLIVVTGNNFDEAASAAHEDARTGATLIBPFDARNVTYIGQGTAAELISQTSMGKAD 196

Db 182 RVFPVGGGGLAAAVAVLIKMLQIKIVIANEADSAICRAALDAGHPVLLPRGLPAEG 241

Db 197 HWVPVGGGGLAGVAVSYMAMARITAVIGIEPGAASMOALHNGPITLETVDPRVDG 256

Qy 242 VAVRIGDETFRLCOEYLDI--ITVDSDAICAMKDLFEDVAVAPSPGALAGMKKY 299

Db 257 AEYKRVGDLNVTYIVKNNQGVHMMASATGAVCTEMLDLYNNEGIAPAPALSIAGKE- 315

Qy 300 IALHNIRGERLANIILSGANVNFHGLRY--VSECELGEOREALLAVTIPEKSGFLKFCQ 357

Db 316 --MSFAPGSVVVCIISGNNDV--LRYAEIERSLVHKGKHYFLVFPQKQRLRHFFLE 371

Qy 358 -LIG-GRSVTEFNY-RPADKNAICIFGVRLSR--GLE---ERKE 394

Db 372 DILGDDDTLCEYLKNNRETGTALVGIHLSASGLDILLERNE 416

RESULT 13

US-09-252-991A-31294

Sequence 31294, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 31294

LENGTH: 374

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-31294

Query Match 19.4%; Score 512; DB 4; Length 374;

Best Local Similarity 32.5%; Pred. No. 2.2e-42;

Matches 119; Conservative 67; Mismatches 134; Indels 46; Gaps 5;

Qy 7 LSGAPGAEYLRVLAAPYVE-----AAQV-----TPLOKMEKLSRLDNVILVKREDR 55

Db 44 LSSLPRSEEPWMDL--PTYDDVIAAARITAGHANRTPVWSSRTLDELGAEVFFKCNL 101

Qy 56 QPVHSPFLRGAVYMMAGLTSEOKAHGIVITASAGNHAQVAFSSARLGKALIVPTATAD 115

Db 102 QRMGAFFRGAFNALSRFSQRAAGVAFSSGNHQAIALSARLIGIPITVMPADAPA 161

Qy 116 IKYDAVAGFGEVILHGANFDEAKAKAIELSQOQFTWVPFDPHVMVIAQGTALALELQ 175

Db 162 VKIEATRGYGQVVLVDRTYEDNEQIGRLAQHGLTILPPYHPVLAQSGRAKELFE 221

Qy 176 QDAHLDRVFPVGGGGLAAVAVLIKMLQIKIVIANEADSAICRAALDAGHPVLLPRV 235

Db 222 EVGPLDAFFAPLGGGGLISGCALAIAPACRIYGVPEAGNDGQSLSGAIVHIDTP 281

Qy 236 GLAEGVAVARIDDEFRLCQEVLDLITVDSALICAMKDLFEDVAVAPSPGALAG 295

Db 282 QTLADGQTOHLNLTFFPLQRVNVDILTASDAELVDGKFLAARKMLIVEPTGCLGLAA 341

Qy 296 MKKYIALHNIRGERLANIILSGANVNFHGLRYVSECELGEOREALLAVTIPEKSGFLK 355

Db 342 ARQ--RKDELKRGKRVGILSGNID-----LARF 368

Qy 356 COLLGG 361

Db 369 CALLGG 374

RESULT 14

US-09-328-352-4536

Sequence 4536, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:



APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 4536  
LENGTH: 328  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-4536

Query Match 17.1%; Score 449.5; DB 4; Length 328;  
Best Local Similarity 34.4%; Pred. No. 2.9e-36;  
Matches 107; Conservative 58; Mismatches 133; Indels 13; Gaps 3;

QY 21 LRAPVYE---AAQ-----VTPLQKMEKLSRLDNVILVREDRQPVHSFKLGAYAM 69  
DB 10 LRLPNVEDVAAAERIKDFINKTPVLTSTVNNNEFAEVEFFKCNFQVGAKEFRGAMNA 69  
QY 70 MAGLIEBQAHGVITTSAGNHAQVAFSSARLGKALVIMPTATADIKVDVARGGCVL 129  
DB 70 LQFNETQKAGVAFSSGNHAQALSSKIIIGIPATIIIPKDPAPAKMAATREYGGNTV 129  
QY 130 LHGANDEAKKAKAIELSQOQGFVTPPFPHPVVIAGGTLALELLOQDAHLDRVFPVVG 189  
DB 130 EEDRYTEDEKIKETAEKNGLLTLPSPHPVVIAGGTAKELEFVGDLDLFPVCLGG 189  
QY 190 GGLAGVAVAILIKQLMPOIKVIAVEADSACLAALDAGHPVDLPRVGLFAEGVAVAKRIGD 249  
DB 190 GGLAGSALSARQLSPKCIYGEPALENDGQWSPFRKGEIVHIDTPPTIADGAQTQYLCK 249  
QY 250 ETPRLCOEYLDITITVDSALICAMKDLFEDVRAVAEPPSGALALAGMKYIALHNI RGER 309  
DB 250 LTFPIIQOQVDDILTVTDEBLINAMKFAERMKVVEPTGCLGFAPAARN--LKDILKGR 307  
QY 310 LAHILSGANVN 320  
DB 308 IGIILSGANDV 318

RESULT 15  
US-09-789-300A-2  
Sequence 2, Application US/0989300A  
Patent No. 6438576  
GENERAL INFORMATION:  
APPLICANT: Meyers, Rachel  
APPLICANT: Rudolph-Owen, Laura A.  
TITLE OF INVENTION: 22406, A No. 6458576el Human Pyridoxal-Phosphate  
FILE REFERENCE: 35800/208926  
CURRENT APPLICATION NUMBER: US/09/789,300A  
CURRENT FILING DATE: 2001-02-20  
PRIOR APPLICATION NUMBER: US 60/183,208  
PRIOR FILING DATE: 2000-02-17  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 340  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-789-300A-2

Query Match 13.6%; Score 357; DB 4; Length 340;  
Best Local Similarity 30.7%; Pred. No. 4.8e-27;  
Matches 93; Conservative 66; Mismatches 134; Indels 10; Gaps 5;

QY 25 VTEAAQVTPLOKMEKLSRLDNVILVREDRQPVHSFKLGAYAMAGLTE---EOKAHG 81  
DB 19 IRDSIHILTPTLSTSIQLTGRNLFKCELFQKTSFKIKGALNAVAISLPDALLERKPKA 78  
QY 82 VITASGNHAQVAFSSARLGKALVIMPTATADIKVDVARGGCVLHGANFDEAKAK 141

DB 79 VVTHSSGNHGALTYAAKLEBGIPIYIVPQTAPOCKKLATQAGASYCEPSDESREN 138  
QY 142 AIELSQOQGFVTPPFPHPVVIAGGTLALELLOQDAHLDRVFPVGGGGLAGVAVILIK 201  
DB 139 AKRTEETEGIMVFNPEPNAVIAOGGTLALEVNLQVPLVDALVVPVGGGGLAGIATVK 198  
QY 202 QLMPOIKVIAVE---AEDSACLKALDAGHPVDLPRVGLFAEGVAVAKRIGDETRLCOEY 258  
DB 199 ALKPSVKVYAAEPENADD--CYQSKLKGKLMPLNLYPPTIADGVK--SSIGLNTWPIIRDL 255  
QY 259 IDITITVDSALICAMKDLFEDVRAVAEPPSGALALAG--MKYIALHNI RGERLAHILSGA 317  
DB 256 VDDIFTVEDEIKCATQULWBERMKLLIPTAGVAVALSQHFOQTVSEPVKNICLVSSG 315  
QY 318 NVN 320  
DB 316 NVD 318

Search completed: December 18, 2003, 15:30:48  
Job time : 22 secs



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QY 1 MADSOPLSGAPGEGAYLRVAVLRAPVYEAQVTPLOQMEKLSRLDNVILVKREDROPVHS 60
DB 1 MADSOPLSGAPGEGAYLRVAVLRAPVYEAQVTPLOQMEKLSRLDNVILVKREDROPVHS 60
QY 61 FKLRGAYAMMAGLTTEOKAHGVTITASAGNHAQGVAFSSARLGVKALIIMPTATADIKVDA 120
DB 61 FKLRGAYAMMAGLTTEOKAHGVTITASAGNHAQGVAFSSARLGVKALIIMPTATADIKVDA 120
QY 121 VRFGEVLLHGANFDEAKAKAIELSQOQGFVWPFPDHPMVIAGGTLAELLQODAH 180
DB 121 VRFGEVLLHGANFDEAKAKAIELSQOQGFVWPFPDHPMVIAGGTLAELLQODAH 180
QY 181 DRFPVVGGGGAGAAVAVILKQMPQIKVIAVEABDSACKALADAGHPVDLPRVGLFAE 240
DB 181 DRFPVVGGGGAGAAVAVILKQMPQIKVIAVEABDSACKALADAGHPVDLPRVGLFAE 240
QY 241 GVAVKRIGDETRLCOEYLDIITVDSDAICAMKDLFEDVRAVAEPPSALALAGMKKYI 300
DB 241 GVAVKRIGDETRLCOEYLDIITVDSDAICAMKDLFEDVRAVAEPPSALALAGMKKYI 300
QY 301 ALHNIRGERLAHILSGANVFHGLRYVSRCELSGEOREALAVTIPEEKGSFLKFCOLLG 360
DB 301 ALHNIRGERLAHILSGANVFHGLRYVSRCELSGEOREALAVTIPEEKGSFLKFCOLLG 360
QY 361 GRSVTEFNFRPADAKNACIFVGVRLSRGLEERKEILOMLNDGYSVVDLSDDMAKLHYR 420
DB 361 GRSVTEFNFRPADAKNACIFVGVRLSRGLEERKEILOMLNDGYSVVDLSDDMAKLHYR 420
QY 421 YWVGGRPSHPLQERLYSFEFPSPGAXLRFLNTLGTWNISLPHYRSHGTDYGRVLAPE 480
DB 421 YWVGGRPSHPLQERLYSFEFPSPGAXLRFLNTLGTWNISLPHYRSHGTDYGRVLAPE 480
QY 481 XGDHEPDPETRLNELGYDCHDETNNPAPRFFLAG 514
DB 481 XGDHEPDPETRLNELGYDCHDETNNPAPRFFLAG 514

RESULT 2
ID Q8FBR4 PRELIMINARY; PRT; 515 AA.
AC Q8FBR4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Threonine dehydratase biosynthetic (EC 4.3.1.19).
GN ILVA OR C4694.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Raske D.J., Buckles E.L., Lion S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Domeneberg M.S., Blatter F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli."
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR EMBL; AE016769; AAN8126.1; -.
KW Lyase; Complete proteome.
SQ SEQUENCE 515 AA; 56285 MM; AF0770496585871 CRC64;

Query Match 99.3%; Score 2615; DB 16; Length 515;
Best Local Similarity 99.0%; Pred. No. 4,4e-174;
Matches 509; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 MADSOPLSGAPGEGAYLRVAVLRAPVYEAQVTPLOQMEKLSRLDNVILVKREDROPVHS 60
DB 2 MADSOPLSGAPGEGAYLRVAVLRAPVYEAQVTPLOQMEKLSRLDNVILVKREDROPVHS 61

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QY 61 FKLRGAYAMMAGLTTEOKAHGVTITASAGNHAQGVAFSSARLGVKALIIMPTATADIKVDA 120
DB 62 FKLRGAYAMMAGLTTEOKAHGVTITASAGNHAQGVAFSSARLGVKALIIMPTATADIKVDA 121
QY 121 VRFGEVLLHGANFDEAKAKAIELSQOQGFVWPFPDHPMVIAGGTLAELLQODAH 180
DB 122 VRFGEVLLHGANFDEAKAKAIELSQOQGFVWPFPDHPMVIAGGTLAELLQODAH 181
QY 181 DRFPVVGGGGAGAAVAVILKQMPQIKVIAVEABDSACKALADAGHPVDLPRVGLFAE 240
DB 182 DRFPVVGGGGAGAAVAVILKQMPQIKVIAVEABDSACKALADAGHPVDLPRVGLFAE 241
QY 241 GVAVKRIGDETRLCOEYLDIITVDSDAICAMKDLFEDVRAVAEPPSALALAGMKKYI 300
DB 242 GVAVKRIGDETRLCOEYLDIITVDSDAICAMKDLFEDVRAVAEPPSALALAGMKKYI 301
QY 301 ALHNIRGERLAHILSGANVFHGLRYVSRCELSGEOREALAVTIPEEKGSFLKFCOLLG 360
DB 302 ALHNIRGERLAHILSGANVFHGLRYVSRCELSGEOREALAVTIPEEKGSFLKFCOLLG 361
QY 361 GRSVTEFNFRPADAKNACIFVGVRLSRGLEERKEILOMLNDGYSVVDLSDDMAKLHYR 420
DB 362 GRSVTEFNFRPADAKNACIFVGVRLSRGLEERKEILOMLNDGYSVVDLSDDMAKLHYR 421
QY 421 YWVGGRPSHPLQERLYSFEFPSPGAXLRFLNTLGTWNISLPHYRSHGTDYGRVLAPE 480
DB 422 YWVGGRPSHPLQERLYSFEFPSPGAXLRFLNTLGTWNISLPHYRSHGTDYGRVLAPE 481
QY 481 XGDHEPDPETRLNELGYDCHDETNNPAPRFFLAG 514
DB 482 XGDHEPDPETRLNELGYDCHDETNNPAPRFFLAG 515

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RESULT 3
ID Q8X467 PRELIMINARY; PRT; 515 AA.
AC Q8X467;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 23, Last annotation update)
DE Threonine deaminase (Dehydratase).
GN ILVA OR Z5283.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blatter F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RT Nature 409:528-533(2001).
RL EMBL; AE005608; AAG58967.1; -.
DR InterPro; IPR001926; B6_enzyme_beta.
DR InterPro; IPR000634; S/T_dehydrtase.
DR InterPro; IPR001721; ThrDh_C.
DR InterPro; IPR005787; Thr_dehydrataseI.
DR Pfam; PF00291; PALP; 1.
DR Pfam; PF00585; Thr_dehydrat_C; 2.
DR TIGRFAMs; TIGR01124; ILVA_2cterm; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
KW Complete proteome.
SQ SEQUENCE 515 AA; 56339 MM; C57C02BE7F17D05F CRC64;

Query Match 97.8%; Score 2575.5; DB 16; Length 515;
Best Local Similarity 98.1%; Pred. No. 2.5e-171;
Matches 505; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

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DR	TIGRFAMs	TTGR01124	11va_2cTerm_1
KM	PROSITE	PS00165	DEHYDRATASE_SER_THR_1
SR	Complete proteome		
SR	SEQUENCE	514 AA	56276 MW; 17B0670DD66E035B CRC64
Qy	Query Match	95.7% Score 2520	DB 16; Length 514
Qy	Best Local Similarity	94.9% Pred. No. 1	9e-167
Db	Matches	488; Conservative 18	Mismatches 8; Indels 0; Gaps 0
Qy	1	MADSOPLSGAPEGAAYLRAVLRAVVEAAQVTPLOKMEKLSRLDNIIVKREDQVHS	60
Db	1	MAESQPSIVAPEGAAYLRAVLRAVVEAAQVTPLOKMEKLSRLDNIIVKREDQVHS	60
Qy	61	FKLRGAYAMMAGLTEEKAKGVITTAAGNNAAGVAFSSALLGVKALIVMPATADIVDA	120
Db	61	FKLRGAYAMMAGLTEEKAKGVITTAAGNNAAGVAFSSALLGVKSLIVMPATADIVDA	120
Qy	121	VREGGGEVVLHGAFNFDPAKAKATELSQOQGFPTWPPDPHVMVLAGOSTLALLETLOQDAHL	180
Db	121	VREGGGEVVLHGAFNFDPAKAKATELSQOQGFPTWPPDPHVMVLAGOSTLALLETLOQDSHL	180
Qy	181	DRVFPVPGGGGLAAGVAVLIKOLMPQIKVIAVEADSDACIKALADGHPVDLPFVGLFAE	240
Db	181	DRVFPVPGGGGLAAGVAVLIKOLMPQIKVIAVEADSDACIKALAEAGHPVDLPFVGLFAE	240
Qy	241	GVAVKRIGDETFRLCQELVDITVDSDAICAMKDLFEDVRAVAEFGALALAGMKKYI	300
Db	241	GVAVKRIGDETFRLCQELVDITVDSDAICAMKDLFEDVRAVAEFGALALAGMKKYI	300
Qy	301	ALHNIRREIRLAHLISGANNVNPHGIRVYSEKCEIGEOREALLAVTIPKESFLKECOLLG	360
Db	301	AQHNIRREIRLAHLISGANNVNPHGIRVYSEKCEIGEOREALLAVTIPKESFLKECOLLG	360
Qy	361	GRSVTEFNYPFADAKNACIFGVYALSRGSEERKEIILQMLNDGYSVVDLSDDENAKLHVR	420
Db	361	GRWTEFNYPFADAKNACIFGVYALSRGSEERKEIITQLCDGYSVVDLSDDENAKLHVR	420
Qy	421	YMWGGRPSHPIQERLYSFEPFESFGAYLRPLNTLGTWNTSLFHYRSHGTDYGVLAFAE	480
Db	421	YMWGGRPSKPIQERLYSFEPFESFGALKEFHTLGTWNTSLFHYRSHGTDYGVLAFAE	480
Qy	481	XGDEHPDEFIRLNLGYDCHDETNPAPRFEEFLAG 514	
Db	481	LGDEHPDEFIRLNLGYECHDESNNPAPRFEEFLAG 514	
RESULT 5			
Q8ZAB4	PRELIMINARY;	PRT;	514 AA.
AC	Q8ZAB4;		
DT	01-MAR-2002 (Tremblere1_20, Created)		
DT	01-MAR-2002 (Tremblere1_20, Last annotation update)		
DT	01-MAR-2003 (Tremblere1_23, Last annotation update)		
DE	Threonine dehydratase (EC 4.2.1.16) (Threonine deaminase).		
GN	ILVA OR YPO3896 OR Y0339.		
OS	Yersinia pestis.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;		
OC	Enterobacteriaceae; Yersinia.		
OX	NCBI_TaxID=612;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CO-92 / Biovar Orientalis;		
RC	MEDLINE=21470413; PubMed=11586360;		
RA	Parkhill J., Sebainia M., Thomson N.R., Tibball R.W., Holden M.T.G.,		
RA	Prentice M.B., Wren B.W., Church C.D., Church C., Mungall K.L.,		
RA	Baker S., Baaham D., Bentley S.D., Brooks K., Cerdano-Tarrega A.M.,		
RA	Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,		
RA	Fellwell T., Hamlin N., Holroyd S., Jagels K., Kariyasev A.V.,		
RA	Leather S., Moutie S., Oyston P.C.F., Quail M., Rutherford K.,		
RA	Simmonds M., Skelton J., Stevens K., Whithead S., Barrall B.G.;		
RT	"Genome sequence of Yersinia pestis, the causative agent of plague,"		
RN	Nature 413:523-527(2001).		
	[2]		

RP SEQUENCE FROM N.A.  
 RC STRAIN-KIMS / Biovar Mediaevallie;  
 RX MEDLINE=2237863; PubMed=12142430;  
 RA Deng W., Burland V., Plunkett G., III, Boutin A., Mayhew G.F., Liss P.,  
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,  
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,  
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,  
 RA Perry R.D.;  
 RT "Genome sequence of *Yersinia pestis* KIM.";  
 RL J. Bacteriol. 184:4601-4611(2002).  
 DR EMBL; AJ414159; CAC93363.1; -.  
 DR EMBL; AF013634; AAM83930.1; -.  
 DR InterPro; IPR001926; B6 enzyme beta.  
 DR InterPro; IPR000634; S/T dehydratase.  
 DR InterPro; IPR001721; ThrDh C.  
 DR InterPro; IPR005787; Thr\_dehydratet.  
 DR Pfam; PF00291; PALE; 1.  
 DR Pfam; PF00585; Thr\_dehydrat C; 2.  
 DR TRIGRAMS; TRIGR01124; 11VA\_2Cterm; 1.  
 DR PROSITE; PS00165; DEHYDRATASE\_SER\_THR; 1.  
 KM Lyase; Complete proteome.  
 SQ SEQUENCE 514 AA; 55935 MW; A49EA796A2CE6640 CRC64;

Query Match 85.4%; Score 2249; DB 16; Length 514;  
 Best Local Similarity 84.2%; Pred. No. 1.5e-148;  
 Matches 433; Conservative 40; Mismatches 41; Indels 0; Gaps 0;

QY 1 MADSQLSGAPBEAEVLRARVYEAQVTPLOKMEKLSRLDNVILVREDRQPVHS 60  
 DB 1 MAVSQPLSAPCAEYLRALRALRAVYEAQVTPLOKMEKLSRVGVTAVKREDROPVHS 60  
 QY 61 FPKRGVYAMAGLTTEOKAHGVTASAGNHAQGVAFSSARLGVKALIMPTATADIKVA 120  
 DB 61 FPKRGVYAMISLTTEOKACGVTTASAGNHAQGVAFSSARLGVKALIMPTATADIKVA 120  
 QY 121 VRGFGSEVLLHGANFDEAKAKAIELSQOQGFVWPPFDHMPVIAAGCTLALELLQDAHL 180  
 DB 121 VRAFGSEVLLHGANFDEAKAKAIALAQEQGYTFVPPFDHMPVIAAGCTLALELLQDAHL 180  
 QY 181 DRFVAVVGGGGLAAGVAVLIKQMLPQIKVIAVEASACIKALADGHPVDLPVGLFPAE 240  
 DB 181 DRFVAVVGGGGLAAGVAVLIKQMLPQIKVIAVEASACIKALADGHPVDLPVGLFPAE 240  
 QY 241 GVAVKRIGDEPRLCOEYLDITVSDAICAMKDLFEDVRAVAPSGALALAGMKKTY 300  
 DB 241 GVAVKRIGDEPRLCOEYLDITVSDAICAMKDLFEDVRAVAPSGALALAGMKKTY 300  
 QY 301 ALANRIGERLAHLISGANVNFHGLRYVSERCLEGEORALAVTIPEEKGSFLKFCOLLG 360  
 DB 301 QQHNIGERLAHLISGANVNFHGLRYVSERCLEGEORALAVTIPEEKGSFLKFCOLLG 360  
 QY 361 GRSVTEFNRYFAADAKNACTVGVRLSGLEERKEIILOMLNDGYSVYDLSDDMAKLHVR 420  
 DB 361 GRSVTEFNRYFAADAKNACTVGVRLSGLEERKEIILOMLNDGYSVYDLSDDMAKLHVR 420  
 QY 421 YWVGSRPSHPLQRIYVSEFPESPGAXLRFLNTLGTWYNISLFYRSHGTDYGRVLAPE 480  
 DB 421 YWVGSRPSHPLQRIYVSEFPESPGAXLRFLNTLGTWYNISLFYRSHGTDYGRVLAPE 480  
 QY 481 XGDHEDPFETRLNELGYDCHDETNPAPFRFLAG 514  
 DB 481 LSATPEQFERLAALGYCHDETNDNPAFKFPLAG 514

RESULT 6  
 Q8DDG2 PRELIMINARY; PRT; 509 AA.  
 AC Q8DDG2;  
 DT 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Threonine dehydratase.  
 GN VV11028.

OS *Vibrio vulnificus*.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxId=672;  
 RN (1)  
 RC SEQUENCE FROM N.A.  
 RC STRAIN-CMC6;  
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,  
 RA Choy H.E.;  
 RT "Complete genome sequence of *Vibrio vulnificus* CMC6.";  
 RL Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AE016800; AA009516.1; -.  
 KM Complete proteome.  
 SQ SEQUENCE 509 AA; 55989 MW; BA29330A31822994 CRC64;

Query Match 71.7%; Score 1888.5; DB 16; Length 509;  
 Best Local Similarity 70.7%; Pred. No. 2.1e-123;  
 Matches 355; Conservative 68; Mismatches 78; Indels 1; Gaps 1;

QY 13 GAETVRAVLRARVYEAQVTPLOKMEKLSRLDNVILVREDRQPVHSFKLAGYAMMAG 72  
 DB 8 GADYLRQILIRARVYEAQVTPLOKMEKLSRLDNVILVREDRQPVHSFKLAGYAMMAG 67  
 QY 73 LTEOKAHGVTASAGNHAQGVAFSSARLGVKALIMPTATADIKVAVRFGSEVLLHG 132  
 DB 68 LSOAQKDGAVITASAGNHAQGVAFSSARLGVKALIMPTATADIKVAVRFGSEVLLHG 127  
 QY 133 ANPDEAKAKAIELSQOQGFVWPPFDHMPVIAAGCTLALELLQDAHLDRVAVPVGCGGL 192  
 DB 128 SNPDEAKAKAIELSQOQGFVWPPFDHMPVIAAGCTLALELLQDAHLDRVAVPVGCGGL 187  
 QY 193 AAGVAVLIKQMLPQIKVIAVEASACIKALADGHPVDLPVGLFPAEGVAVKRGDETF 252  
 DB 188 AAGVAVLIKQMLPQIKVIAVEASACIKALADGHPVDLPVGLFPAEGVAVKRGDETF 247  
 QY 253 RLCOEYLDITVSDAICAMKDLFEDVRAVAPSGALALAGMKKTYALANRIGERLAH 312  
 DB 248 RLCOEYLDITVSDAICAMKDLFEDVRAVAPSGALALAGMKKTYALANRIGERLAH 307  
 QY 313 IISGANVNFHGLRYVSERCLEGEORALAVTIPEEKGSFLKFCOLLGSRSTEFNRYRA 372  
 DB 308 VLSGANVNFHGLRYVSERCLEGEORALAVTIPEEKGSFLKFCOLLGSRSTEFNRYRA 367  
 QY 373 DAKNACIFGVVLSGLEERKEIILOMLNDGYSVYDLSDDMAKLHVRWVGSRPSHPLQ 432  
 DB 368 DQSLANIFGVVLSGLEERKEIILOMLNDGYSVYDLSDDMAKLHVRWVGSRPSHPLQ 427  
 QY 433 ERLYSEFPESPGAXLRFLNTLGTWYNISLFYRSHGTDYGRVLAPEXGDHE-PDFETR 491  
 DB 428 ERLYSEFPESPGAXLRFLNTLGTWYNISLFYRSHGTDYGRVLAPEXGDHE-PDFETR 487  
 QY 492 LNELGYDCHDETNPAPFRFLA 513  
 DB 488 LRELGYQCKDVTNDPSYRFFLS 509

RESULT 7  
 Q9KRW1 PRELIMINARY; PRT; 510 AA.  
 AC Q9KRW1;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-OCT-2000 (Tremblrel. 22, Last annotation update)  
 DE Threonine dehydratase.  
 GN VC0027.  
 OS *Vibrio cholerae*.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxId=666;  
 RN (1)  
 RC SEQUENCE FROM N.A.  
 RC STRAIN-EI Tor N16961 / Serotype O1;  
 RX MEDLINE=20406833; PubMed=10952301;

RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,  
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,  
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,  
 RA Ermolaeva M.D., Vamathevan J., Baas S., Qin H., Dragoi I., Sellers P.,  
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,  
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
 RA Fraser C.M.;  
 RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*  
 RT *cholerae*";  
 RL Nature 406:477-483(2000).  
 DR EMBL; AE004094; AAF93205.1; -.  
 DR HSSP; P04968; 1TDJ.  
 DR TIGR; VC0027; -.  
 DR InterPro; IPR001926; B6 enzyme beta.  
 DR InterPro; IPR000634; S/P dehydratase.  
 DR InterPro; IPR001721; ThnD.C.  
 DR InterPro; IPR005787; Thn dehydratase.  
 DR Pfam; PF00291; PALP; 1.  
 DR Pfam; PF00585; Thn dehydratase C; 2.  
 DR TIGRfam; TIGR01124; llyA 2Cterm; 1.  
 DR PROSITE; PS00165; DEHYDRATASE\_SER\_THR; 1.  
 KM Complete proteome.  
 SQ SEQUENCE 510 AA; 56173 MW; 0690875549B38C25 CRC64;

Query Match 70.2%; Score 1849.5; DB 16; Length 510;  
 Best Local Similarity 70.2%; Pred. No. 1,1e-120;  
 Matches 354; Conservative 64; Mismatches 81; Indels 5; Gaps 2;

QY 13 GAETLRAVLRAVYEAQVTPLOKMEKLSRLDNLVLRERDQVHSPFKLRGAYAMAG 72  
 DB 8 GAETLRAVLRAVYEAQVTPLOKMEKLSRLDNLVLRERDQVHSPFKLRGAYAMAG 67  
 QY 73 LTBEGKAGVITASAGNAGVAFSARLVKALIVMTATADIVDAVRGEGVLLHG 132  
 DB 68 LTBEGKAGVITASAGNAGVAFSARLVKALIVMTATADIVDAVRGEGVLLHG 127  
 QY 133 ANPEAKAKATLSSQOGFTWVPDPHPIVAGGTLALTELLQODAHIDRVFVPGGGGL 192  
 DB 128 SNPEAKAKATLSSQOGFTWVPDPHPIVAGGTLALTELLQODAHIDRVFVPGGGGL 187  
 QY 193 AAGVAVLIKQMPQIKVIAVEADSAKLAALDAGHPVDLPVGLFAEGVAVKRIIDET 252  
 DB 188 AAGVAVLIKQMPQIKVIAVEADSAKLAALDAGHPVDLPVGLFAEGVAVKRIIDET 247  
 QY 253 RLCEYLDITTVSDAICAMKLPEDVRAVAESGALALAGMKKATLAINIRGERLAH 312  
 DB 248 RLCEYLDITTVSDAICAMKLPEDVRAVAESGALALAGMKKATLAINIRGERLAH 307  
 QY 313 ILSGANVPHGLRYVSECEGEORALLAVTIPREKSPFLKCOLLGRSVTEPNYRFA 372  
 DB 308 VLSGANVPHGLRYVSECEGEORALLAVTIPREKSPFLKCOLLGRSVTEPNYRFA 367  
 QY 373 DAKNAQIFVGYRLSGLEERKEILQMLNDGYSVVDLSDDEMAKLVHVMVGGPRSHPLQ 432  
 DB 368 DQQLANITVGYRLVGGPDELKSIHILRQSGVPVDDLSDDEMAKLVHVMVGGPRSHPLQ 427  
 QY 433 ERLVSFEPESPQAKLRFLNTLGTIYWNISLFHYRSHGTDYGRVLAFAFGDHEP---PE 489  
 DB 428 ERLVSFEPESPQAKLRFLNTLGTIYWNISLFHYRSHGTDYGRVLAFAFGDHEP---PE 485  
 QY 490 TRINELGYDCHDETNNPAPRFLLA 513  
 DB 486 EHLVELGYRYKDETDNPAIRFLLA 509

RESULT 8  
 Q8E9E0 PRELIMINARY; PRT; 545 AA.  
 AC Q8E9E0.  
 DT 01-MAR-2003 (TREMblrel. 23, Created)  
 DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Threonine dehydratase.

GN llyA OR SC04344.  
 OS *Shewanella oneidensis*.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
 OC Alteromonadales; *Shewanella*.  
 OC NCBI\_TaxID=70863;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MR-1;  
 RX MEDLINE=22297686; PubMed=12368813;  
 RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,  
 RA Read T.D., Eisen J.A., Seehardt R., Ward N., Methe B., Clayton R.A.,  
 RA Meyer T., Tsaplin A., Scott J., Beanan M., Brinkac L., Daugherty S.,  
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,  
 RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,  
 RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,  
 RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,  
 RA Feldblyum T.V., Smith H.O., Venter J.C., Nelson K.H., Fraser C.M.;  
 RT "Genome sequence of the dissimilatory metal ion-reducing bacterium  
 RT *Shewanella oneidensis*";  
 RL Nat. Biotechnol. 20:1118-1123(2002).  
 DR EMBL; AE015867; AAN57312.1; -.  
 DR TIGR; SO4344; -.  
 KM Complete proteome.  
 SQ SEQUENCE 545 AA; 58971 MW; 5CD1A85B4C95B3 CRC64;

Query Match 58.9%; Score 1550; DB 16; Length 545;  
 Best Local Similarity 58.0%; Pred. No. 9.4e-100;  
 Matches 304; Conservative 86; Mismatches 120; Indels 14; Gaps 4;

QY 2 ADSQPLSGAEGAE-----YLRAVLRAVYEAQVTPLOKMEKLSRLDNLVLRERD 54  
 DB 12 AESQPLSGAEGAE-----YLRAVLRAVYEAQVTPLOKMEKLSRLDNLVLRERD 71  
 QY 55 RQPVHFKLRGAYAMAGLTBEQKAGVITASAGNAGVAFSARLVKALIVMTATADIV 114  
 DB 72 MQPVHFKLRGAYAMAGLTBEQKAGVITASAGNAGVAFSARLVKALIVMTATADIV 131  
 QY 115 DIKVDARVGLGAGVITLHGANDFAKATLSSQOGFTWVPDPHPIVAGGTLALTELL 174  
 DB 132 DIKVDARVGLGAGVITLHGANDFAKATLSSQOGFTWVPDPHPIVAGGTLALTELL 191  
 QY 175 QQDADLRVFPVGGGGLAGVAVLIKQMPQIKVIAVEADSAKLAALDAGHPVDLP 234  
 DB 192 QQDADLRVFPVGGGGLAGVAVLIKQMPQIKVIAVEADSAKLAALDAGHPVDLP 251  
 QY 235 VGLFAEGVAVKRIIDETFRLCQEYLDITTVSDAICAMKLPEDVRAVAESGALALA 294  
 DB 252 VGLFAEGVAVKRIIDETFRLCQEYLDITTVSDAICAMKLPEDVRAVAESGALALA 311  
 QY 295 GMKRYIALH-----NIRGERLAHILSGANVPHGLRYVSECEGEORALLAVTIPREK 350  
 DB 312 GLKRYVSTNATGESGREGKVAALLISGANVPHGLRYVSECEGEORALLAVTIPREK 371  
 QY 351 SFLKFCOLLGGRSVTEPNYRPAADAKNACIFVGYRLSGLEERKEILQMLNDGYSVVDL 410  
 DB 372 SFLKFCOLLGGRSVTEPNYRPAADAKNACIFVGYRLSGLEERKEILQMLNDGYSVVDL 431  
 QY 411 DDENAKLVHVMVGGPRSHPLQERLYSFEPEPQAKLRFLNTLGTIYWNISLFHYRSHG 470  
 DB 432 GDETAKLHVMVGGPRSHPLQERLYSFEPEPQAKLRFLNTLGTIYWNISLFHYRSHG 491  
 QY 471 DYGRVLAFAFGDHEP---PE 512  
 DB 492 AFGRVLAFAFGDHEP---PE 534

RESULT 9  
 Q9I4I8 PRELIMINARY; PRT; 515 AA.  
 AC Q9I4I8.  
 DT 01-MAR-2001 (TREMblrel. 16, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)

DE Threonine dehydratase, biosynthetic.  
GN TLV42 OR PA1326.  
OS *Pseudomonas aeruginosa*.  
OC *Bacteria*; *Proteobacteria*; *Gamma proteobacteria*; *Pseudomonadales*;  
OC *Pseudomonadaceae*; *Pseudomonas*.  
ON NCBI\_TaxID=287;  
RX [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 15692 / PAOI;  
RX MEDLINE=20437337; PubMed=10984043;  
RA Stever C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
RA Hickey M.J., Brinkman F.S.L., Huffnagle W.O., Kowalik D.J., Lagrou M.,  
RA Bradley R.L., Gentry L., Tolentino E., Westbrock-Wadman S., Yan Y.,  
RA Gorder L.L., Coulter S.N., Folger K.R., Kas A., Larity K., Lim R.M.,  
RA Smith K.A., Spencer D.H., Mong G.K.-S., Wu Z., Paulsen I.T.,  
RA Reizner J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.,  
RT "Complete genome sequence of *Pseudomonas aeruginosa* PAOI, an  
RT opportunistic pathogen".  
RL Nature 406:959-964 (2000).  
DR EMBL; AE004562; AAC04715.1; -.  
DR HSSP; P04968; 1TDJ.  
DR InterPro; IPR001926; B6 enzyme\_beta.  
DR InterPro; IPR000634; S/T dehydratase.  
DR InterPro; IPR001121; ThrDn\_C.  
DR InterPro; IPR005787; Thr\_dehydratase.  
DR Pfam; PF00291; PALP; 1.  
DR Pfam; PF00585; Thr dehydrat C; 2.  
DR TIGRFAMs; TIGR01124; tlva\_2Ctem; 1.  
DR PROSITE; P800165; DEHYDRATASE\_SER\_THR\_1.  
KW Complete proteome.  
SQ SEQUENCE 515 AA; 55903 MW; D06F9C512C791E19 CRC64;

Query	Match	Similarity	54.4%	Pred.	No.2.1e-90,	Matches	279;	Conservative	95;	Indels	7;	Gaps	3
QY	1	MADSOPLSGAPEAGYELRAVLRA	PAPYEAAQVLPLOKMEKLSRLNVILVKREDOPYHS	60									
DB	6	LSASRPL-----	AGYVESILLA	PAPYDVAVERFLPQAOLSRLOGRNVILVKREDLOPFS	60								
QY	61	EKLRAGYVMAGLTTEEOKAHGVIT	SAGNHAQVAPSSARLGVALLIMPTATADI	KODA	120								
DB	61	FKIRGAYTRVA	LSBOKARGVIT	SAGNHAQGLLAQRLGVRAVITVMPRTTPELKVYG	120								
QY	121	VRGEGEVILH	QANDEKAKAIEISQOQGF	WVBPDPHBMVIT	IAOGTALTELLQO-DAH	179							
DB	121	VLAARGEALH	HDAPPDALAHLLQLAERGMF	FVPPYDDPDVIAQGYAMKILKOHSGR	180								
QY	180	LDRVAVPVGGGI	LAAGVAVL	LKQMLPOLVIA	AVEADBSACLKAALDAGHPVDL	PRVGLFA	239						
DB	181	LDATVVPVGGSL	LIAGIAVYVHKL	LPDIRIVIGVEPEBDSCLQALALAGRRVVL	GGVGLFA	240							
QY	240	BGVAVKRI	IGDETFRLCOEYLD	DIITVDSDAICAMKDL	FEDEVRAVAEP	SGALALAGMKY	299						
DB	241	DGVAVAQIGAC	NFCVCKDHVDE	VITVSGDEICAAIKDIYD	TRSTTEP	PAGALAVAGIKKY	300						
QY	300	IATNHIRGER	LHILISGANVNF	HGRLRYSERCELEB	QORALLAVIT	PEKSGFLFCOLL	359						
DB	301	VARETEQOT	VAIDSGANIN	FDRLRHVAERLELB	QORALLAVITVAVERP	SGFKAFCAAL	360						
QY	360	GRSVTEF	FNYPADAKNACIF	VGVALSRLEJERKEILLQ	LVNDGYSVDL	SDENAKLHV	419						
DB	361	GRQOTTER	NYRKHSDROAHL	PLVGVOTHP	PLTDSRADL	LAGLRQGGFPVLDL	TINBAKKLHI	420					
QY	420	RYMVGG	RSPHLOERLYS	FEPESPQAKMLR	PLNTLGT	YWNISLFYHRSHTDY	GYVLAAF	479					
DB	421	RHMVGCH	TEVVRERLFR	PEPPEP	PCOALLNF	DKLGRWNISL	LFYHNRHGAD	GRVLAGL	480				
QY	480	EXGDHE	-PDFETRLNEL	GDCHDE	TNNPAFRFF	511							
DB	481	QVPDERGE	LEALALQAI	GYPMVEE	ETNNPAFRFF	513							

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RESULT 10
09JUX5
ID 09JUX5 PRELIMINARY; PRT; 508 AA.
AC 09JUX5.
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Putative chorone dehydratase biosynthetic (Ec 4.2.1.16).
GN tiva OR NMA1096.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Baaham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jazels K., Leather S., Moulé S., Mungall K.M., Simmonds M., Skelton J.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RL meningitidis Z2491."
RL Nature 404:502-506(2000).
RR EMBL; AL162755; CABB4359.1; -.
RR HSSP; P04968; 1TDJ.
DR InterPro; IPR001926; B6_enzyme_beta.
DR InterPro; IPR000634; S/T_dehydrtse.
DR InterPro; IPR001721; ThnDh_C.
DR InterPro; IPR005787; Thr_dehydratasei.
DR Pfam; PF00291; PALP; 1.
DR Pfam; PF00585; Thr_dehydrat_C_2.
DR TIGRfams; TIGR01124; tiva_2Cterm; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
KW Lyase; Complete proteome.
SQ SEQUENCE 508 AA; 55212 MW; DBA1BAFC6A9332E CRC64;

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[illegible]



Db	Accession	Length	Score	DB	Length	Score	DB
Db	425 ENERLVSEPFPERPQALRALFLNMHGCGNNITLFYHRNNGADYGRILVIGDVPHPDAAFD	484					
Qy	490 TRINAEIGYDCHDETNPAFRPFLA	513					
Db	485 GFLESLGYSYHEETONAAVKLFLLA	508					
RESULT 11							
Q9JZW1	PRELIMINARY;	PRT;	508 AA.				
AC	Q9JZW1						
DT	01-OCT-2000 (Tremblrel. 15, Created)						
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)						
DT	01-OCT-2002 (Tremblrel. 22, Last annotation update)						
DE	Theonine dehydratase.						
GN	NMB0878.						
OS	Neisseria meningitidis (serogroup B).						
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;						
OC	Neisseriaceae; Neisseria.						
OX	NCBI_Taxid=491;						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=MC58 / Serogroup B;						
RC	MEDLINE=20175755; PubMed=10710307;						
RA	Tetteijn H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,						
RA	Eisen J.A., Ketchum K.A., Hood D.W., Pedon J.F., Dodson R.J.,						
RA	Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,						
RA	Hatt D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,						
RA	Maeson T., Cleekzo A., Parksey D.S., Blair E., Clitome H., Clark E.B.,						
RA	Cotton M.D., Ulteback T.R., Khouti H., Qin H., Vamathevan J.,						
RA	Gill J., Scarlatte V., Maignan V., Pizze M., Grandi G., Sun L.,						
RA	Smith H.O., Fraser C.M., Moxon E.R., Rappunli R., Venter J.C.;						
RT	"Complete genome sequence of Neisseria meningitidis serogroup B strain						
RT	MC58."						
RL	Science 287:1809-1815 (2000).						
RL	EMBL; AE002440; AAF41289.1; -.						
DR	HSSP; P04968; 1TDJ.						
DR	TIGR; NMB0878; -.						
DR	InterPro; IPR001926; B6 enzyme beta.						
DR	InterPro; IPR000634; S/F dehydratase.						
DR	InterPro; IPR001721; Thrdh_C.						
DR	InterPro; IPR005787; Thr_dehydratase.						
DR	Pfam; PF00291; PALP; 1.						
DR	Pfam; PF00585; Thr_dehydratase C; 2.						
DR	TIGRFAMS; TIGR01124; llyA_2Cterm; 1.						
DR	PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.						
KW	Complete proteome.						
SO	SEQUENCE 508 AA; 55192 MW; 087DB8CF41810353 CRC64;						
Query Match	53.2%; Score 1400.5; DB 16; Length 508;						
Best Local Similarity	55.0%; Pred. No. 2.3e-89;						
Matches	277; Conservative 89; Mismatches 131; Indels 7; Gaps 4						
Qy	14 AEYLRAVLRAPYEAQVTPLOKMEKLSRLDNVILVKKREDQPYHSEFLRGAYMMAGL	73					
Db	8 SDYLIRLITASYDVAVETPELEPARSLVLRKNNILLKREDLQPVFSFKIRGAYKMSKL	67					
Qy	74 TEEQAAHGVITTSAGNHAQGVAFSSARLGVKALLYMPATATADIKYDAYRGFGCVLLNGA	133					
Db	68 PKDALACGVIAASQNHQGVASLQRLGCRVIVYMPETTPKIKYDAYVSHGSEVLLNGV	127					
Qy	134 NFDEAKAIAIEISQOQGFVWPFPDPHVMVIAQGTALTELLQQDAAHLD---RVFVPVGG	190					
Db	128 SYNDAYDVAMELAEAGLITVIAFPDDPVIYAGQGVGMEIVSQ--HPDDIRAVFPIGG	185					
Qy	191 GIAAGVAVILKQMLPQIKVIAVEADSDACKALDAGHPVDLPRVGLFAEGVAVRIGDE	250					
Db	186 GIAAGVAAFIKQVREIKVIGVQTNDSCMKOSVEAGEIVLHLKDVGLFSDGTAVYVGNRE	245					
Qy	251 TFRLOEYVDLITVYDSADICAAAMDLPEDVAVVAPESSGALLAAGKKYITALHNIRGRT	310					
Db	246 TFRLLKELLDELITVYDIDVAVCAVNDIPDQTSITTEPRALLAAGIKAYIAEGGAEQNTL	305					

Qy	311	AHILSGANVNPHGRVYSERCELEQORFALLAAVTIPEEKSGFLKRCOLLGSGSVTEPNR	370
Db	306	IATVSGANMNRHLRHHYSEKSELGEGNEGTRAVIIPERKSGFLKRVNLTGNRNITEFNR	365
Qy	371	FADAKNACIFVGNVLSRGLERKEIQLMTLNDGYSVVDLSDDEMAKLVHRYVMVGRPSHP	430
Db	366	YGDDEKHHIFVGLQ-AGGPODLAVIIGSLDDEAGLPVNDLTNNELAKIHRIYVWGRTDKV	424
Qy	431	LOERLYSEFEPESFGAKIRPLNTLGTWNISLFHYRSGTIDYGRVLAAPKXDBE-PDPE	489
Db	425	ENELVSEFEPEREGALARFLFNHNGGWNITLTFHYRNHGADYGRVLGIDVPPHDAADF	484
Qy	490	TRNLNELGYDCHDETNNPAREFLA 513	
Db	485	GFLSLGYSYHEETONAAVYKFLFA 508	
RESULT 12			
Q9RMU8			
ID	Q9RMU8	PRELIMINARY;	PRT; 568 AA.
AC	Q9RMU8;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)		
DE	Theonine dehydratase, biosynthetic.		
GN	DR0567.		
OS	Deinococcus radiodurans.		
OC	Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;		
CC	Deinococcaceae; Deinococcus.		
OX	NCBI_TaxID=1299;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=R1;		
RX	MEDLINE=20036896; PubMed=10567266;		
RA	White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,		
RA	Whitson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,		
RA	Madson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,		
RA	Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,		
RA	Vamatheva J.J., Lam P., McDonald L., Utechtack T., Zalewski C.,		
RA	Marakovan K.S., Aaravind L., Daly M.J., Manton K.W., Fleischmann R.D.,		
RA	Kechum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,		
RA	Frazer C.M.;		
RT	"Genome sequence of the radioresistant bacterium Deinococcus		
RT	radiodurans R1."		
RL	Science 286:1571-1577(1999).		
DR	EMBL; AE001915; AAF10147.1; -.		
DR	HSSP; P04968; 1TDJ.		
DR	TIGR; DR0567; -.		
DR	InterPro; IPR001926; B6_enzyme_beta.		
DR	InterPro; IPR001721; TnDh_C.		
DR	InterPro; IPR005787; Tn_dehydratEI.		
DR	Pfam; PF00291; PALP; 1.		
DR	Pfam; PF00585; Thr_dehydrat_C; 2.		
DR	TIGRFAMS; TIGR01124; 1lva_2ctem; 1.		
KM	Complete proteome.		
SQ	SEQUENCE 568 AA; 61321 MW; DBA0A1A946DAC1F CRC64;		
Query Match 52.4%; Score 1380.5; DB 16; Length 568;			
Best Local Similarity 53.8%; Pred. No. 6,7e-88;			
Matches 276; Conservative 92; Mismatches 134; Indels 11; Gaps 4			
Qy	6	PLSGAPGAEYLRARVYEAQVTPQLQKMKLSSRLDNVILYKREDROPVHSFKLG 65	
Db	60	PLPGTLDMVDVLRLLTQGVYGAATETPLSPAPRLSESGNVLKREDOQPIFSFKLG 119	
Qy	66	AYANMAGLTREQKAGVITASAGNNAQVARSASATLGYKALIVMPATADIVDVAVRG 125	
Db	120	AYNKSQSLAERARAGVICASGNNAQGVAFGEKLGIPAVIVMPATPDIYQACRAG 179	
Qy	126	GEVLHAGNPDDEAKAKATELSQOQFTWVPPRPHVNVIAQGTALLETLODANDL-RVF 184	
Db	180	AEVILHNGSFDALFETALALQGERELTGVHYPDRLVLAQGTALLETLLRQVEEDYAVF 239	
Qy	185	VPVGGGGLAGVAVILIKOLMPOIKVIAVEADSDACKAALDNGHVPVDLPRVGLFAEGVAV 244	

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DB 240 VEVGGGGLIAGVAAIILKALKPGRVIGVPPDDSDANYOSILOAGERVRLDTVGI FVGVAV 299
QY 245 KRIIGDEFTLCOEYLDITVDSDAICAMKDLFEEDVAVAPSPGALATAGKKYATALHN 304
DB 300 KQGVATFTLTRYVDWVRVNDVCALIKDFDTRAVLEBAGLSVAGLKRTAATNG 359
QY 305 IGERLAHLISGANVNFGLRYVSECELGEOREALLAVTIBEKSGFLKFCOLLGSRV 364
DB 360 LHDRTLVALTCGINIFDLRHVAERTELIGEOREALITVTPERPGAFLEFIELGSRAT 419
QY 365 TERNTRFADAKNACIVGVRLSRGLERKEIILQMLNDGYSVVDLSDDMAKLTFRYMG 424
DB 420 TERNRYAPREDRIFVGVOLGQP-GEROBLTLILNGRGYAVDLTDEDELAHVHMHMG 478
QY 425 GRPSHLOERLVSFEPPSPGAXLRFINTLGTWNTSLFHYRSHGTDYGRVLAAPSGDH 484
DB 479 GRAPPAVNERVYAFVTPPERGALHDFLTOLQGEWNTSLFHYRSHGSAHGRVLAGVQV--- 535
QY 485 EPD----FETRLNELGYDCHDETNNPAPRFPL 512
DB 536 -PDALTRFGDFLAGLGYPAHDVTSNPAYRFL 567

RESULT 13
QY16G0 PRELIMINARY; PRT; 504 AA.
AC 0916G0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Threonine dehydratase, biosynthetic.
GN ILVAT OR PA0331.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RA MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kae A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.,
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
DR EMBL: AE004471; AAC03720.1; -
DR HSSP: P04968; ITDU.
DR InterPro: IPR001926; B6 enzyme beta.
DR InterPro: IPR000634; S/T dehydratase.
DR InterPro: IPR001721; ThrDh C.
DR InterPro: IPR005787; Thr dehydratase.
DR Pfam: PF00291; PALP; 1.
DR TIGRFAMs: TIGR01124; IlyA_2Cterm; 1.
DR PROSITE: PS00165; DEHYDRATASE_SER_THR; 1.
KW Complete proteome.
SQ SEQUENCE 504 AA; 55351 MW; 055CEFA3E5A18D73 CRC64;

Query Match 51.4%; Score 1354; DB 16; Length 504;
Best Local Similarity 52.6%; Pred. No. 3.9e-86;
Matches 263; Conservative 95; Mismatches 140; Indels 2; Gaps 2;
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DB 64 BEERKGVIAASAGNHAOCGLAALAKRGIRAVIYMPKTTPEIKVOAVRAHAKAVLHGD 123
QY 125 FDEAKAKAIEISOOQGFVTPDFDHPMVIAQGTALBEL-QODAHLDVFPVGGGLA 193
DB 124 FPEALAHKLVDKSGYTFVHPYDDPDTIAGGTVAIMEILQQPRLDAIFVVGGLV 183
QY 194 AGVAVLILQMLPQIVIAVEADSACLKALDAGHPVLPRVGLFAEGVAYKRIDETFR 253
DB 184 AGIAVYVYLPEIKVIVIEVPEPESNCLQAMAAAGRRVVLGVGVFADGVAAAOIQHTFD 243
QY 254 LCOEYLDITVDSDAICAMKDLFEEDVAVAPSPGALATAGKKYATALHNIGERLAHI 313
DB 244 ICKDHVDEITVSTDEICAIIDITDTRSTIEPGALAVAGIKYVERBERAEGTLVAI 303
QY 314 LSGANVNFGLRYVSECELGEOREALLAVTIBEKSGFLKFCOLLGSRVTEFNYPAD 373
DB 304 DSGANVNFGLRYVSECELGEOREALLAVTIBERKREIILQMLNDGYSVVDLSDDMAKLTFRYMG 363
QY 374 AKNACIFGVRLSRGLERKEIILQMLNDGYSVVDLSDDMAKLTFRYMGGRPSHLOE 433
DB 364 GSEAHIFVGVQTHPENDEPREALVAYLREKGPVLDLTNNEIAKLIIRHVGSHAVKVSDE 423
QY 434 RLVSFEPPSPGAXLRFINTLGTWNTSLFHYRSHGTDYGRVLAAPSGDHEDPD-FETRL 492
DB 424 MVRFPFPPRGALFNFLTKLGRNNISWFRNHGAADGRVAGLQVPEDERHLIPQTL 483
QY 493 NELGYDCHDETNNPAPRFPL 512
DB 484 EALGYPMWDETANPAYQLFL 503

RESULT 14
QY16G2 PRELIMINARY; PRT; 503 AA.
AC 08YPG2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Threonine dehydratase.
GN ALR4232.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriuguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohata M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.,
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL: AP003595; BAB75931.1; -
DR InterPro: IPR001926; B6 enzyme beta.
DR InterPro: IPR000634; S/T dehydratase.
DR InterPro: IPR001721; ThrDh C.
DR InterPro: IPR005787; Thr dehydratase.
DR Pfam: PF00291; PALP; 1.
DR TIGRFAMs: TIGR01124; IlyA_2Cterm; 1.
DR PROSITE: PS00165; DEHYDRATASE_SER_THR; 1.
KW Complete proteome.
SQ SEQUENCE 503 AA; 56026 MW; D9F6FCB4480348 CRC64;

Query Match 50.1%; Score 1318.5; DB 16; Length 503;
Best Local Similarity 50.2%; Pred. No. 1.2e-83;
Matches 251; Conservative 106; Mismatches 140; Indels 3; Gaps 3;
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Qy 75 EEOKAHVITASAGNHAQVAFSSARLGKALVIMPTATADIKYDAVRGEGEVLHGAN 134
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 64 PDLLAQGVITASAGNHAQVAFSSARLGKALVIMPTATADIKYDAVRGEGEVLHGDT 123
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 135 FDEAKAKAIELSQOQGTWPPEFDHPVIAQGTALATELLQO-DAHLDREVFPVGGGLA 193
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 YDDAYAVARQLEAEKGLTFIHPDDPHVIAQGTALATELLQOQPHAFVAILGGGLI 183
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 194 AGVAVLTKQMPQIKVIAVEBEDSACLKALDAGHPVDLPVVGFAEGVAVKRGDETER 253
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 SGIAAYVAVKRLPEIKIGVEPVDADAMQSLQAKRVRVLSQVGFAGGVAVRVEGEFTR 243
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 254 LCOEYLDITVDSDAICAAKMDLFEDVRAVAEPPSGALALAGMKKYLALHNIRGERLAI 313
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 LCOEYVBEIITVDITDAICAAKMDLVFODTRSLTEPAGALALAGKQYAADRKLSQSL 303
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 314 LSGANVPHGLRVYSERCGEORALLAVTIPEKGSFLKCOLLGRSVTEFENYRPAD 373
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 304 ACGANMFPDRLRFVAERAEFGERREAIFAVTIPEPSLRFKCECIGRRNLTEFNRIAD 363
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 374 AKNACTIVGVLRLSGERKEILQMLNDGYSVDLSDEMAKLVHRYVGGRSHPLOE 433
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 364 EKIHIFIGMGI-QNRADKIMVETFAECGEIIDLTDDELTKLRLRMVGGHSPLANE 422
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 434 RLVSFEPSPGAXLRFNLTLGTWNISLFHYRSHGTDYGRVLAFAEXGDHE-DFETRL 492
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 423 LLYFPEPPERGALMKFVASMSPNNISLFHYRNNGSDYGRIVGMQVPOEMEMQWFL 482
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 493 NELGYDCHDETNNPAFRFL 512
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 483 DSLGYQWDESDQNPAYKFL 502
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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## RESULT 15

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ID Q8Y287 PRELIMINARY; PRT; 507 AA.
AC Q8Y287;
DT 01-MAR-2002 (TREMblrel. 20. Created)
DT 01-MAR-2002 (TREMblrel. 20. Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22. Last annotation update)
DE Probable chreonine dehydratase (Threonine deaminase) transmembrane
   protein (EC 4.2.1.16).
GN ILVA OR RSC0449 OR RS04453.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
   OC Ralstoniaceae; Ralstonia.
OX NCB1_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
   Ariat M., Billaut A., Broctier P., Camus J.C., Catolico L.,
   Chandler M., Choisme N., Claudel-Renard C., Cunac S., Demange N.,
   Gaepin C., Lavie M., Moisan A., Robert C., Saurin W., Schiek T.,
   Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
   Weissenbach J., Boucher C.A.;
RA "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RT Nature 415:497-502(2002).
RL EMBL; AL646059; CAD13977.1; -.
DR InterPro; IPR001926; B6_enzyme_beta.
DR InterPro; IPR000634; S/T_dehydrtase.
DR InterPro; IPR001721; TnDh_C.
DR InterPro; IPR005787; Thr_dehydratase.
DR Pfam; PF00291; PALP; 1.
DR Pfam; PF00585; Thr_dehydratase; 2.
DR TIGRFAMs; TIGR01124; ILVA_2Cterm; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
KW Lyase; Complete proteome.
SQ SEQUENCE 507 AA; 5566 MW; 1C7A04667BC5F644 CRC64;

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Query Match 49.7%; Score 1307.5; DB 16; Length 507;

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Best Local Similarity 51.8%; Pred. No. 7e-83;
Matches 263; Conservative 90; Mismatches 140; Indels 15; Gaps 6;
Qy 15 EYLRVAVRAVYEAQVTPYQKMEKSSRLDNVILVREEROPHPSFKLGAYMMGLT 74
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4 DYLRKILYAVYDVAAQETDLPAPSLRIGNRYYLRENOQPFPSFKLGAYMMGLT 63
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 75 EEOKAHVITASAGNHAQVAFSSARLGKALVIMPTATADIKYDAVRGEGEVLHG 131
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 64 PAERKGVITASAGNHAQVAFSSARLGKALVIMPTATADIKYDAVRGEGEVLHG 123
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 132 GANFDEAKAKAIELSQOQGTWPPEFDHPVIAQGTALATELLQOQAH-LDRVFPVGG 190
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 GESYTDYDAVAVKLEHGHTFVHPDDPVIAGQGTIAVEILRQHPHPIAIPALIGG 183
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 191 GLAAGVAVLTKQMPQIKVIAVEBEDSACLKALDAGHPVDLPVVGFAEGVAVKRGDE 250
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 GLVSGIAAYVAVKRPDIKVGOTADSDAMACSVAAKRVTLRDVGLPSDGTAVKLVGKE 243
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 251 TFRLOEYLDITVDSDAICAAKMDLFEDVRAVAEPPSGALALAGMKKYLALHNIRGERL 310
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 TFRLTRVBEIITVDITDAICAAKMDLVFODTRSLTEPAGALALAGKQYAADRKLSQSL 303
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 311 AHLISGANVPHGLRVYSERCGEORALLAVTIPEKGSFLKCOLLGRSVTEFENY 369
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 304 VALISGANMFPDRLRFVAERAEVGEAREAVAVTIPEPERSFRFCVVGSRVTEFENY 363
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 370 RFDARAKACTIVGVLRLSGERKEILQMLNDGYSVDLSDEMAKLVHRYVGG 425
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 364 RIDKNEAHIFVGVQVLSRAEGDK----IADGRKRGFPFLDLSNDELAKOHIRYVGG 418
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 426 RPSHPLQERLYSFEPPSPGAXLRFNLTLGTWNISLFHYRSHGTDYGRVLAFAEXGDHE 485
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 419 HSPLAENELLYRPFEPERPGALITFLSSMSBNNISLFHYRNQADSNNILVGIQVRNE 478
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 486 P-DFETRLNELGYDCHDETNNPAFRFL 512
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 479 KRAFKAFATLGLYTFMDESENPAVYGLFL 506
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Job time : 42 secs

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